

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 30, 2005, 15:43:12 ; Search time 94 Seconds
(without alignments)

1364.985 Million cell updates/sec

Title: US-10-035-958-61

Perfect score: 1204

Sequence: 1 MGMTMLVTAALLGLMMVV.....PTLQAPGRASEPKHTRQR 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Uniprot 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1196	99.3	223	1	BPPL_HUMAN
2	561.5	46.6	242	1	PEPL_MOUSE
3	260.5	21.6	211	2	Q86PT6
4	258.5	21.5	224	2	Q7QHW0
5	246	20.4	214	2	Q7PWN1
6	236	19.6	191	2	Q7PVP6
7	235.5	19.6	186	1	PEBP_RAT
8	235.5	19.6	187	2	AAH63171
9	234.5	19.5	221	1	BPBH_CAEEL
10	231	19.2	152	1	D1_ONCVO
11	231	19.2	179	2	Q6J0U4
12	231	19.2	179	2	AAT38121
13	229	19.0	257	2	Q9VR60
14	225	18.7	186	1	PEBP_MOUSE
15	223	18.5	134	1	D3_ONCVO
16	222.5	18.5	187	2	Q9V108
17	222	18.4	197	1	OV16_ONCVO
18	219	18.2	114	1	D2_ONCVO
19	218.5	18.1	186	1	PEBP_BOVIN
20	218.5	18.1	187	1	PEB2_MOUSE
21	216.5	18.0	202	2	Q9V109
22	213.5	17.7	187	2	Q6NTS4
23	213.5	17.7	187	2	AAH66479
24	211.5	17.6	187	2	Q8MK57
25	210.5	17.5	187	2	Q7ZUV8
26	206	17.1	186	1	PEBP_MACFA
27	205	17.0	173	1	NFT_ARATH
28	205	17.0	186	1	PEBP_HUMAN
29	203	16.9	121	2	Q9D9I9
30	202	16.8	186	2	Q6GPR7
31	199	16.5	135	2	Q8TAK8

32	199	16.5	186	2	Q6IRM0
33	199	16.5	186	2	AAH70868
34	197.5	16.4	241	2	Q7PYP5
35	196	16.3	171	2	Q9NKY4
36	195	16.2	178	2	Q84XL1
37	194.5	16.2	241	2	Q7QHV9
38	192.5	16.0	173	2	Q6LSN9
39	187.5	15.6	177	2	Q84XL0
40	186.5	15.5	179	2	Q9VD02
41	186	15.4	174	2	Q76EQ5
42	186	15.4	174	2	BAD01612
43	186	15.4	174	2	BAD08338
44	185	15.4	174	2	Q76CC3
45	185	15.4	174	2	BAD01561
46	185	15.4	174	2	BAD08337
47	185	15.4	178	2	Q8VMH2
48	183	15.2	172	2	Q9XW37
49	183	15.2	174	2	Q6R3R0
50	183	15.2	174	2	Q76BW3
51	183	15.2	174	2	AAS00056
52	183	15.2	174	2	BAD02372
53	183	15.2	177	1	BFT_ARATH
54	182	15.1	175	1	TSF_ARATH
55	182	15.1	179	2	Q93W19
56	182	15.1	179	2	Q93WM7
57	181.5	15.1	211	2	Q917L3
58	181	15.0	210	1	OBAS_DROME
59	179	14.9	177	2	Q9SX79
60	177.5	14.7	176	2	Q6XHR8
61	177.5	14.7	176	2	AAH10138
62	175.5	14.6	174	2	Q9ASJ1
63	175.5	14.6	176	2	Q9VD01
64	175	14.5	174	2	Q76CA4
65	175	14.5	174	2	BAD01576
66	173	14.4	185	2	Q6EUF9
67	172	14.3	174	2	Q76BM4
68	172	14.3	174	2	BAD02371
69	169.5	14.1	262	1	TE26_TOXCA
70	168.5	14.0	175	2	Q84XK9
71	168	14.0	151	2	Q70JR7
72	168	14.0	151	2	CAE53888
73	168	14.0	173	2	Q75QM9
74	168	14.0	173	2	BAD08339
75	166.5	13.8	173	2	Q75QX2
76	166	13.8	174	2	Q75QW8
77	166	13.8	174	2	BAD08340
78	165.5	13.7	173	2	Q7XAB3
79	164.5	13.7	176	2	Q9FTP7
80	164	13.6	174	1	CET1_TOBAC
81	164	13.6	175	1	FT_ARATH
82	164	13.6	175	2	AAH38819
83	164	13.6	175	2	AAH91747
84	162.5	13.5	194	2	Q6CFV4
85	162	13.5	229	2	Q7QAQ7
86	160.5	13.3	172	2	Q84XK7
87	160	13.3	174	2	Q7XUF1
88	159	13.2	182	2	Q9Y1K8
89	155.5	12.9	212	2	Q6BS89
90	154.5	12.8	173	2	Q9XGS4
91	154	12.8	145	2	Q70JR8
92	154	12.8	145	2	CAE53887
93	153.5	12.7	174	2	Q6VG98
94	153.5	12.7	174	2	AAH03725
95	152	12.6	173	2	Q9XGS5
96	152	12.6	174	2	Q6LSU7
97	152	12.6	174	2	Q6TXM3
98	152	12.6	174	2	Q76FW2
99	152	12.6	174	2	AAQ88444
100	152	12.6	174	2	BAD01610
101	152	12.6	174	2	BAD01611
102	150	12.5	172	2	Q76M79
103	150	12.5	172	2	BAD06418
104	150	12.5	175	2	Q6BS90

Q6IRM0 xenopus lae	Q6IRM0
Aah70868 xenopus l	AAH70868
Q7PYP5 anopheles g	Q7PYP5
Q9NKY4 dirofilaria	Q9NKY4
Q84XL1 lycopseico	Q84XL1
Q7QHV9 anopheles g	Q7QHV9
Q6LSN9 populuss nig	Q6LSN9
Q84XL0 lycopseico	Q84XL0
Q9VD02 drosophila	Q9VD02
Q76EQ5 populuss nig	Q76EQ5
BAD01612 populuss n	BAD01612
BAD08338 populuss n	BAD08338
Q76CC3 populuss nig	Q76CC3
BAD01561 populuss n	BAD01561
BAD08337 populuss n	BAD08337
Q8VMH2 oryza sativ	Q8VMH2
Q9XW37 caenorhabdi	Q9XW37
Q6R3R0 populuss del	Q6R3R0
Q76BW3 populuss nig	Q76BW3
AAS00056 populuss d	AAS00056
BAD02372 populuss n	BAD02372
Q9SX79 arabidopsis	Q9SX79
BFT_ARATH	BFT_ARATH
TSF_ARATH	TSF_ARATH
Q93W19 oryza sativ	Q93W19
Q93WM7 oryza sativ	Q93WM7
Q917L3 drosophila	Q917L3
P54185 drosophila	P54185
Q9SX79 citrus unsh	Q9SX79
Q6XHR8 drosophila	Q6XHR8
AAH10138 drosophila	AAH10138
Q9ASJ1 oryza sativ	Q9ASJ1
Q9VD01 drosophila	Q9VD01
Q76CA4 populuss nig	Q76CA4
BAD01576 populuss n	BAD01576
Q6EUF9 oryza sativ	Q6EUF9
Q76BM4 populuss nig	Q76BM4
BAD02371 populuss n	BAD02371
TE26_TOXCA	TE26_TOXCA
Q84XK9 lycopseico	Q84XK9
Q70JR7 triticum ae	Q70JR7
CAE53888 triticum	CAE53888
Q75QM9 populuss nig	Q75QM9
BAD08339 populuss n	BAD08339
Q75QX2 populuss nig	Q75QX2
Q75QW8 malus domes	Q75QW8
BAD08340 malus dom	BAD08340
Q7XAB3 pisum sativ	Q7XAB3
Q9FTP7 oryza sativ	Q9FTP7
Q9XN44 nicotiana t	Q9XN44
Q9SX22 arabidopsis	Q9SX22
AAH38819 arabidops	AAH38819
AAH91747 arabidops	AAH91747
Q6CFV4 varrowia li	Q6CFV4
Q7QAQ7 anopheles g	Q7QAQ7
Q84XK7 lycopseico	Q84XK7
Q7XUF1 oryza sativ	Q7XUF1
Q9Y1K8 octopussy dof	Q9Y1K8
Q6BS89 debaryomyce	Q6BS89
Q9XGS4 oryza sativ	Q9XGS4
Q70JR8 triticum ae	Q70JR8
CAE53887 triticum	CAE53887
Q6VG98 pisum sativ	Q6VG98
Q9XGS5 oryza sativ	Q9XGS5
Q6LSU7 populuss nig	Q6LSU7
Q6TXM3 populuss trl	Q6TXM3
Q76FW2 populuss nig	Q76FW2
AAQ88444 populuss t	AAQ88444
BAD01610 populuss n	BAD01610
BAD01611 populuss n	BAD01611
Q76M79 malus domes	Q76M79
BAD06418 malus dom	BAD06418
Q6BS90 debaryomyce	Q6BS90

105	148.5	12.3	175	1	SP_LYCSES	O82088 lycopersico	178	106	8.8	181	2	Q7NTA2	Q7nta2 chromobacte
106	148	12.3	181	1	CEN_ANTMA	Q41261 antirrhinum	179	105.5	8.8	105	2	Q84MI7	Q84mi7 vitis vinif
107	147.5	12.3	175	1	CET2_TOBAC	Q9xh43 nicotiana t	180	105	8.7	198	1	Y6G9_PYRHO	O58984 pyrococcus
108	147	12.2	175	1	CEN_ARATH	Q9xh43 arabidopsis	181	104	8.6	152	2	Q988D1	Q988d1 rhizobium l
109	147	12.2	175	2	AAM15187	Aam15187 arabidops	182	104	8.6	182	2	Q2Q6Q3	Q2q6q3 salmonella
110	147	12.2	175	2	AAL38687	Aal38687 arabidops	183	103.5	8.6	58	2	Q7Y1X3	Q7y1x3 arabidopsis
111	147	12.2	175	2	AAM20165	Aam20165 arabidops	184	103.5	8.6	177	2	Q9ADN9	Q9adn9 streptomyce
112	145	12.0	204	2	Q751Y1	Q751y1 ashbya goss	185	103	8.6	354	2	Q6C3U0	Q6c3u0 yarrowia li
113	145	12.0	204	2	AAS54066	Aas54066 ashbya go	186	103	8.6	416	2	Q9VY48	Q9vy48 drosophila
114	144.5	12.0	175	1	CET4_TOBAC	Q9xh42 nicotiana t	187	101.5	8.4	150	2	Q821P9	Q821p9 chlamydomo
115	143.5	11.9	105	2	Q96KD0	Q96kd0 homo sapien	188	101.5	8.4	177	2	Q871W2	Q871w2 vibrio para
116	143	11.9	173	2	O8L1M8	O8llm8 vitis vinif	189	100	8.3	183	2	Q7C164	Q7c164 shigella fl
117	142.5	11.8	177	2	O8LSG7	O8lsg7 arabidopsis	190	100	8.3	183	2	Q83KN3	Q83kn3 shigella fl
118	141	11.7	173	2	Q6L5U5	Q6l5u5 populus nig	191	100	8.3	183	2	Q8CVY8	Q8cvy8 escherichia
119	140	11.6	173	2	Q6ESF8	Q6esf8 oryza sativ	192	100	8.2	216	2	Q9HND1	Q9hnd1 halobacteri
120	139.5	11.6	140	2	O84XK8	O84xk8 lycopersico	193	98.5	8.2	191	2	Q8KET2	Q8ket2 chlorobium
121	138	11.5	173	2	Q9XH41	Q9xh41 nicotiana t	194	98	8.1	91	2	Q6VG97	Q6vg97 pisum sativ
122	138	11.5	173	2	Q7XVG4	Q7xvg4 oryza sativ	195	98	8.1	91	2	AAR03726	Aar03726 pisum sac
123	137.5	11.4	177	1	TEFL1_ARATH	P93003 arabidopsis	196	97.5	8.1	210	2	Q6D4D5	Q6dd4d5 erwinia car
124	137.5	11.4	177	2	O8LSH9	O8lsh9 arabidopsis	197	96.5	8.0	150	1	Y877_CHLPN	Q92729 chlamydia p
125	137.5	11.4	177	2	O8LSH9	O8lsh9 arabidopsis	198	96.5	8.0	177	2	Q9FB60	Q9fb60 corynebacte
126	137.5	11.4	177	2	AAM27943	Aam27943 arabidops	199	96.5	8.0	346	2	Q8X2M0	Q8x2m0 mus musculu
127	137.5	11.4	177	2	AAM27944	Aam27944 arabidops	200	96.5	8.0	346	2	Q99LM1	Q99lm1 mus musculu
128	137.5	11.4	177	2	AAM27945	Aam27945 arabidops	201	96	8.0	239	2	Q94J24	Q94j24 oryza sativ
129	137.5	11.4	177	2	AAM27946	Aam27946 arabidops	202	96	8.0	345	2	Q6NWB9	Q6nwb9 brachydan
130	137.5	11.4	177	2	AAM27948	Aam27948 arabidops	203	96	8.0	345	2	AAH67649	Aah67649 brachydan
131	137.5	11.4	177	2	AAM27949	Aam27949 arabidops	204	95.5	7.9	290	2	O8BTZ1	Q8btz1 mus musculu
132	137.5	11.4	177	2	AAM27950	Aam27950 arabidops	205	95	7.9	169	2	Q92TT5	Q92tt5 rhizobium m
133	137.5	11.4	177	2	AAM27951	Aam27951 arabidops	206	95	7.9	183	1	YBCL_ECOLI	Q92tt5 escherichia
134	137.5	11.4	177	2	AAM27954	Aam27954 arabidops	207	95	7.9	205	1	YJ11_MYCTU	P77368 streptomyce
135	137.5	11.4	177	2	AAM27955	Aam27955 arabidops	208	94.5	7.8	417	2	Q7QEH4	Q6bkh0 debrayomyce
136	137.5	11.4	177	2	AAM27956	Aam27956 arabidops	209	93.5	7.8	157	2	Q9UXF4	Q8kjc6 thauera aro
137	137.5	11.4	190	1	PBP_PLAFA	P54189 plasmodium	210	93.5	7.8	186	1	YB53_PYRAB	Q7qeh4 anopheles g
138	137.5	11.4	190	2	AAD55781	Aad55781 plasmodiu	211	93	7.7	180	2	Q9XT30	Q9uxj3 pyrococcus
139	137.5	11.4	190	2	AAN36277	Aan36277 plasmodiu	212	92	7.6	179	1	YH94_STRCO	Q9kc30 vibrio chol
140	137.5	11.4	190	2	Q6TDS5	O6tds5 lotus japon	213	92	7.6	206	2	AAS03955	Q9x328 streptomyce
141	133	11.0	174	2	AAN33599	Aa93599 lotus japon	214	92	7.6	206	2	Q8XTT0	Q29979 archaeoglob
142	133	11.0	174	2	Q9SAY4	Q9say4 brassica ol	215	91.5	7.6	159	2	SYE_ARCFU	Q829c7 streptomyce
143	133	11.0	178	2	O82152	O82152 brassica na	216	91.5	7.6	551	1	Q829C7	Q6bkh0 debrayomyce
144	133	11.0	178	2	Q9SAY5	Q9say5 brassica na	217	91	7.6	393	2	Q6BKHO	Q8kjc6 thauera aro
145	133	11.0	178	2	Q9SAY5	Q9say5 brassica na	218	91	7.5	209	2	Q74MM9	Q74mm9 nanoarchaea
146	133	11.0	201	1	YL79_YEAST	O82153 brassica ca	219	90.5	7.5	179	2	AAR39014	Aar39014 nanoarcha
147	131	10.9	178	2	O82153	Q9xgd4 dictyosteli	220	90	7.5	179	2	YLA0_MYCTU	O06235 mycobacteri
148	131	10.9	178	2	Q9XGD4	Q9xgd4 dictyosteli	221	89.5	7.4	176	1	Q96DV4	Q96dv4 homo sapien
149	131	10.9	203	2	Q86RH8	Q86rh8 candida gla	222	89.5	7.4	346	2	Q81M99	O8im99 drosophila
150	130	10.8	210	2	Q6FX79	Q6fx79 candida gla	223	89.5	7.4	1505	2	PTPV_MOUSE	P70289 mus musculu
151	129.5	10.8	177	2	O8LSG8	O8lsg8 arabidopsis	224	89.5	7.4	1705	1	Q96681	Q96681 drosophila
152	129.5	10.8	197	2	Q6CUM6	Q6cuw6 kluyveromyc	225	89.5	7.4	1945	2	Q9V491	Q9v491 drosophila
153	128	10.6	173	2	Q9FUA6	Q9fua6 lolium pere	226	89.5	7.4	194	2	Q8PUD5	Q8pud5 methanosarc
154	127	10.5	190	2	Q7RNG5	Q7rng5 plasmodium	227	88.5	7.4	426	2	Q8ETI7	Q8et17 oceanobacil
155	122.5	10.2	219	1	CFY1_YEAST	P14306 saccharomyc	228	88.5	7.4	159	2	Q8EJ20	Q8ej20 shewanella
156	121	10.0	178	2	Q9SAY6	Q9say6 brassica na	229	88.5	7.4	346	2	Q61SR5	Q61s5 oryza sativ
157	117	9.7	168	2	Q7QN27	Q7qn27 anopheles g	230	88	7.3	159	2	Q9P0B9	Q9p0b9 homo sapien
158	115	9.6	202	2	O8ML68	O8ml68 drosophila	231	88	7.3	161	2	Q21608	Q21608 caenorhabdi
159	114	9.5	177	2	O82154	O82154 brassica ol	232	88	7.3	387	2	Q6DB35	Q6db35 erwinia car
160	113.5	9.4	58	2	O84LD8	O84ld8 metrosidero	233	87.5	7.3	251	2	Q6ERK5	Q6erk5 mus musculu
161	113.5	9.4	181	2	Q8NEW7	Q8nbw7 rhodopsudo	234	87.5	7.3	1705	2	Y109_CHLMU	O9pl10 chlamydia m
162	113.5	9.4	181	2	CAE26153	Caetz6153 rhodopeu	235	87	7.2	150	1	Y736_CHLTR	O84711 chlamydia t
163	113.5	9.4	201	1	XJ10_MYCTU	O07723 mycobacteri	236	86.5	7.2	150	1	Q6NH78	Q6nh78 corynebacte
164	113	9.4	149	2	Q975D2	Q975d2 sulfolobus	237	86.5	7.2	179	2	CAE49794	Caetz6153 rhodopeu
165	113	9.4	151	1	Y273_METHH	O26373 methanobact	238	86.5	7.2	1114	2	Q7U236	Q7u236 rhodopirell
166	113	9.4	244	2	Q9P6X9	Q9p6x9 neurospora	239	86	7.1	438	2	Q8L5T3	Q8l5t3 chlamydia m
167	110.5	9.2	154	2	Q92G37	Q92g37 rickettsia	240	85	7.1	438	2	Q813K8	Q813k8 bacillus ce
168	109.5	9.1	58	2	Q84LD7	Q84ld7 metrosidero	241	85.5	7.1	483	2	Q8H0B8	Q8h0b8 triticum ae
169	109.5	9.1	145	2	Q82LW8	Q82lw8 picrophilus	242	85.5	7.1	430	1	ACM4_CHICK	Ac8088 triticum ae
170	108.5	9.0	143	2	Q82XS1	Q82xs1 nitrosomona	243	85	7.1	165	2	Q8Y271	Q8y271 ralsconia s
171	108.5	9.0	181	2	Q72MW8	Q72mw8 leptospira	244	85	7.1	243	2	O8Y271	O8y271 ralsconia s
172	108.5	9.0	181	2	Q8EZL4	Q8ezl4 leptospira	245	85	6.9	757	2	O6CLJ6	O6clj6 kluyveromyc
173	108.5	9.0	181	2	AA571620	Aa571620 leptospir	246	83.5	6.9	857	2	Q746A8	Q746a8 thermus the
174	106.5	8.8	179	2	Q7MCG5	Q7mcg5 vibrio vuln	247	83.5	6.9	857	2	AA582477	Aa582477 thermus t
175	106.5	8.8	179	2	Q8D514	Q8d514 vibrio vuln	248	83.5	6.9	3251	2	AA582477	Aa582477 thermus t
176	106.5	8.8	203	2	Q8TQV5	Q8tqv5 methanosarc	249	83.5	6.9	3251	2	AA582477	Aa582477 thermus t
177	106	8.8	171	1	YC50_AQUAE	O67293 aquifex aeo	250	83	6.9	595	1	SNX9_HUMAN	Q9y5x1 homo sapien

251	83	6.9	2253	2	P700112	P700112 xenopus lae	324	77.5	6.4	1411	2	Q73Y53	Q73Y53 mycobacteri
252	82.5	6.9	420	2	O873115	O873115 mycobacteri	325	77.5	6.4	1411	2	AAS04421	AAS04421 mycobacte
253	82	6.8	176	2	Q9CC45	Q9CC45 mycobacteri	326	77.5	6.4	1564	2	O6DFB8	O6DFB8 xenopus lae
254	82	6.8	198	2	O6I629	O6I629 oryza sativ	327	77.5	6.4	2473	2	Q7QB76	Q7QB76 anopheles g
255	82	6.8	911	2	O9P2J7	O9P2J7 homo sapien	328	77	6.4	235	2	Q87BY4	Q87BY4 xylella fas
256	82	6.8	1072	2	O70EK8	O70EK8 homo sapien	329	77	6.4	455	2	AAM66987	AAM66987 arabidops
257	82	6.8	1072	2	CAE47751	CAE47751 homo sapi	330	77	6.4	1622	1	DNM1_RAT	Q2330 rattus norv
258	81.5	6.8	164	2	Q9FS18	Q9FS18 hordeum vil	331	76.5	6.4	237	2	O8U3G8	Q8U3G8 pyrococcus
259	81.5	6.8	177	2	Q8NQB5	Q8NQB5 corynebacte	332	76.5	6.4	298	2	O9FC20	O9FC20 streptomyce
260	81.5	6.8	177	2	CAE21532	CAE21532 corynebac	333	76.5	6.4	306	2	O7W7L2	O7W7L2 bordetella
261	81.5	6.8	289	2	O6HJS7	O6HJS7 bacillus th	334	76.5	6.4	306	2	O7W7L2	O7W7L2 bordetella
262	81.5	6.8	289	2	O81RJ2	O81RJ2 bacillus an	335	76.5	6.4	360	2	O7V467	O7V467 prochloroco
263	81.5	6.8	289	2	AAT31166	AAT31166 bacillus	336	76.5	6.4	376	2	Q9L8R0	Q9L8R0 s tdp-4-oxo
264	81.5	6.8	421	2	O7TUU6	O7TUU6 prochloroco	337	76.5	6.4	376	2	Q8Z393	Q8Z393 salmonella
265	81.5	6.8	813	2	Q8VUN9	Q8VUN9 streptococc	338	76.5	6.4	382	2	O83C49	O83C49 coxiella bu
266	80.5	6.7	177	2	O8FTC4	O8FTC4 corynebacte	339	76.5	6.4	434	2	Q9Y593	Q9Y593 homo sapien
267	80.5	6.7	287	1	YG98_ARCFU	O28575 archaeoglob	340	76.5	6.4	482	2	O7SH12	O7SH12 nemospora
268	80.5	6.7	370	2	O9LVE7	O9LVE7 arabidopsis	341	76.5	6.4	482	2	CAE76251	CAE76251 neurospor
269	80.5	6.7	495	2	O84W11	O84W11 arabidopsis	342	76.5	6.4	534	2	Q47070	Q47070 escherichia
270	80.5	6.7	533	2	Q9FT21	Q9FT21 arabidopsis	343	76.5	6.4	1159	2	O6DIP9	O6DIP9 xenopus tro
271	80.5	6.7	1032	2	O7IY05	O7IY05 listeria mo	344	76.5	6.4	1206	1	BUN2_DROME	Q24523 drosophila
272	80.5	6.7	1032	2	AAT04810	AAT04810 listeria	345	76.5	6.4	1329	2	Q73TD8	Q73TD8 mycobacteri
273	80	6.6	176	2	O73Y50	O73Y50 mycobacteri	346	76.5	6.4	1329	2	AAS06330	AAS06330 mycobacte
274	80	6.6	176	2	AAS04202	AAS04202 mycobacte	347	76.5	6.4	1955	2	Q7QEM6	Q7QEM6 anopheles g
275	80	6.6	359	2	O6DBN8	O6DBN8 arabidopsis	348	76	6.3	130	1	APAG_RHOPA	Q6N012 rhodopsedo
276	80	6.6	464	2	Q9LTO3	Q9LTO3 arabidopsis	349	76	6.3	130	2	CAE30210	CAE30210 rhodopsesu
277	80	6.6	577	2	O6MHR2	O6MHR2 bdellovibri	350	76	6.3	349	2	O7N747	O7N747 photorhabdu
278	80	6.6	577	2	CAE78270	CAE78270 bdellovib	351	76	6.3	362	2	O8C9S4	O8C9S4 mus musculu
279	80	6.6	625	2	O6GQ13	O6GQ13 xenopus lae	352	76	6.3	410	2	O81AN7	O81AN7 bacillus ce
280	80	6.6	1557	2	O874V8	O874V8 podospora a	353	76	6.3	463	2	Q9RNN3	Q9RNN3 zymomonas m
281	79.5	6.6	300	2	O6DCL2	O6DCL2 xenopus lae	354	76	6.3	748	1	MEPA_RAT	Q4230 rattus norv
282	79.5	6.6	328	2	O95611	O95611 homo sapien	355	76	6.3	857	2	Q9FR78	Q9FR78 oryza sativ
283	79.5	6.6	595	1	SNX9_MOUSE	O91VH2 mus musculu	356	76	6.3	917	2	O8CJC0	O8CJC0 mus musculu
284	79.5	6.6	702	2	O9AN74	O9AN74 bradyrhizob	357	76	6.3	1415	2	O6PD88	O6PD88 brachydanio
285	79.5	6.6	702	2	O79UK7	O79UK7 bradyrhizob	358	76	6.3	1415	2	AAS58868	AAS58868 brachydan
286	79	6.6	352	2	O72H38	O72H38 thermus the	359	76	6.3	1430	2	Q9VX86	Q9VX86 drosophila
287	79	6.6	352	2	AAS81999	AAS81999 thermus t	360	76	6.3	2378	2	O6RKE4	O6RKE4 cochllobolu
288	79	6.6	1004	1	YD83_SCHPO	Q10408 schizosacch	361	76	6.3	2378	2	AAR90265	AAR90265 cochllobolu
289	78.5	6.5	162	2	Q9M042	Q9M042 arabidopsis	362	75.5	6.3	218	2	O8T4N0	O8T4N0 glossina mo
290	78.5	6.5	278	2	O8PCJ7	O8PCJ7 xanthomonas	363	75.5	6.3	275	1	PTXC_PSEST	O69053 pseudomonas
291	78.5	6.5	397	1	TEXT_CHICK	O79778 gallus gall	364	75.5	6.3	427	2	O9RHZ6	O9RHZ6 alicyclobac
292	78.5	6.5	417	2	Q7QB51	Q7QB51 anopheles g	365	75.5	6.3	563	2	Q91N44	Q91N44 bovine vira
293	78.5	6.5	677	2	O8R251	O8R251 mus musculu	366	75.5	6.3	627	2	Q926L2	Q926L2 listeria in
294	78.5	6.5	715	1	SYM_METWA	O9P7J4 methanobarc	367	75.5	6.3	634	2	O8GRU0	O8GRU0 oryza sativ
295	78.5	6.5	805	2	O6CYR7	O6CYR7 erwinia car	368	75.5	6.3	844	2	O81767	O81767 arabidopsis
296	78.5	6.5	1069	2	O8CB37	O8CB37 mus musculu	369	75.5	6.3	1032	2	Q92929	Q92929 listeria in
297	78.5	6.5	1102	1	P11G_PIG	O02697 sus scrofa	370	75.5	6.3	1101	1	P11G_HUMAN	P11G_HUMAN
298	78	6.5	278	2	O6P0Z9	O6P0Z9 brachydanio	371	75.5	6.3	1102	2	Q9BZC8	Q9BZC8 homo sapien
299	78	6.5	278	2	AAS65349	AAS65349 brachydan	372	75.5	6.3	1419	2	O6D375	O6D375 erwinia car
300	78	6.5	305	2	Q76Y33	Q76Y33 bacteriopho	373	75.5	6.3	2035	1	F38A_HUMAN	F38A_HUMAN
301	78	6.5	305	2	AAQ17932	AAQ17932 bacterioph	374	75	6.2	257	2	O8KGU0	O8KGU0 rhizobium l
302	78	6.5	345	2	O7RU21	O7RU21 neurospora	375	75	6.2	267	2	O8XV04	O8XV04 ralistonia s
303	78	6.5	390	2	O9P3C0	O9P3C0 neurospora	376	75	6.2	654	2	O8GJ44	O8GJ44 clostridium
304	78	6.5	454	1	APR2_ARATH	P92981 a 5'-adenyl	377	75	6.2	670	2	O7MT53	O7MT53 porphyromon
305	78	6.5	1105	2	O6FT57	O6FT57 candida gla	378	75	6.2	826	2	O8E1J1	O8E1J1 shewanella
306	78	6.5	1976	2	O8DKR5	Q8DKR5 vibrio vuln	379	75	6.2	862	2	Q22354	Q22354 caenorhabdi
307	77.5	6.4	158	2	O9APQ9	O9APQ9 uncultured	380	75	6.2	980	1	BOB1_YEAST	BOB1_YEAST
308	77.5	6.4	169	2	O74LE6	O74LE6 lactobacill	381	75	6.2	1041	1	EGT2_YEAST	EGT2_YEAST
309	77.5	6.4	169	2	AAS08221	AAS08221 lactobaci	382	75	6.2	1091	2	O6C0R5	O6C0R5 kluyveromyc
310	77.5	6.4	170	2	O9UVY0	O9UVY0 pneumocysti	383	75	6.2	1419	2	Q9V7K0	Q9V7K0 drosophila
311	77.5	6.4	170	2	O9CKV1	O9CKV1 pasteurella	384	75	6.2	1638	2	Q9N8E7	Q9N8E7 trypanosoma
312	77.5	6.4	185	2	O70CAN5	Q70CAN5 streptococc	385	75	6.2	3041	2	Q7SGH3	Q7SGH3 neurospora
313	77.5	6.4	185	2	Q935T5	Q935T5 streptococc	386	74.5	6.2	148	2	O81EM1	O81EM1 bacillus ce
314	77.5	6.4	185	2	CAE52364	CAE52364 streptoco	387	74.5	6.2	278	2	O8PPA5	O8PPA5 xanthomonas
315	77.5	6.4	264	2	O7S9A3	O7S9A3 neurospora	388	74.5	6.2	291	2	Q7ZVD1	Q7ZVD1 brachydanio
316	77.5	6.4	278	2	O8C9N9	O8C9N9 mus musculu	389	74.5	6.2	301	2	O8C183	O8C183 mus musculu
317	77.5	6.4	306	2	O7VV17	O7VV17 bordetella	390	74.5	6.2	451	2	O6NY93	O6NY93 brachydanio
318	77.5	6.4	328	2	O9CXX0	O9CXX0 mus musculu	391	74.5	6.2	451	2	Q7ZW80	Q7ZW80 brachydanio
319	77.5	6.4	391	2	O9XAU0	O9XAU0 rhodococcus	392	74.5	6.2	451	2	AAH66691	AAH66691 brachydan
320	77.5	6.4	391	2	O93DN3	O93DN3 rhodococcus	393	74.5	6.2	454	2	Q9TZC6	Q9TZC6 caenorhabdi
321	77.5	6.4	534	2	O46778	O46778 escherichia	394	74.5	6.2	564	2	Q7QQ92	Q7QQ92 giardia lam
322	77.5	6.4	1130	1	REPT_MOUSE	P97347 mus musculu	395	74.5	6.2	680	2	O52644	O52644 ruminococcu
323	77.5	6.4	1159	2	Q7ZVM1	Q7ZVM1 brachydanio	396	74.5	6.2	686	1	IFL2_HUMAN	IFL2_HUMAN

397	74.5	6.2	688	2	Q7RY86	Q7ry86 neurospora	470	73.5	6.1	2627	2	Q9C0H4	Q9c0h4 homo sapien
398	74.5	6.2	889	2	Q7UYD6	Q7uyd6 rhodopirell	471	73.5	6.1	3770	2	Q869R6	Q869r6 dictyosteli
399	74.5	6.2	1009	2	Q7PUK9	Q7puk9 anopheles g	472	73	6.1	186	2	Q84UX0	Q84ux0 oryza sativ
400	74.5	6.2	1036	2	Q8Y5P1	Q8y5p1 listeria mo	473	73	6.1	255	2	Q6NLM6	Q6nlm6 drosophila
401	74.5	6.2	1098	2	Q6NTI2	Q6nti2 brachydanio	474	73	6.1	255	2	AAS77430	Aas77430 drosophila
402	74.5	6.2	1098	2	AAH68983	Aah68983 brachydan	475	73	6.1	287	2	Q8N8P2	Q8n8p2 homo sapien
403	74.5	6.2	1134	2	Q6PFT5	Q6pft5 brachydanio	476	73	6.1	314	2	Q55493	Q55493 synchocyst
404	74.5	6.2	1134	2	AAH57425	Aah57425 brachydan	477	73	6.1	338	2	Q7S603	Q7s603 neurospora
405	74.5	6.2	1394	2	Q8MST1	Q8mst1 drosophila	478	73	6.1	415	2	Q6VGV2	Q6vgv2 human adeo
406	74.5	6.2	1402	2	Q6FZM0	Q6fzm0 bartonella	479	73	6.1	415	2	AAQ19292	Aaq19292 human ade
407	74.5	6.2	1511	2	Q7QAA3	Q7qaa3 anopheles g	480	73	6.1	446	2	Q80TG3	Q80tg3 mus musculu
408	74.5	6.2	1511	2	Q7VB21	Q7vb21 drosophila	481	73	6.1	452	2	Q9SCX8	Q9sgx8 arabidopsis
409	74.5	6.2	2607	1	BACB_BACLI	Q68007 bacillus li	482	73	6.1	458	1	BPHA_PSEPS	Q52028 pseudomonas
410	74	6.1	148	2	Q7BG5	Q7bg5 thermoplasma	483	73	6.1	458	1	Q9AEY5	Q9aey5 pseudomonas
411	74	6.1	159	2	Q7O585	Q7o585 anopheles g	484	73	6.1	524	2	Q9G6W1	Q9g6w1 aspergillus
412	74	6.1	172	2	Q6KIK7	Q6kik7 mycoplasma	485	73	6.1	533	1	TX15_HUMAN	Q96af7 homo sapien
413	74	6.1	172	2	AAI27569	Aat27569 mycoplasma	486	73	6.1	547	2	Q9X058	Q9x058 thermocoga
414	74	6.1	190	2	Q8RZH8	Q8rzh8 oryza sativ	487	73	6.1	585	2	Q8TXG6	Q8txg6 methanopyru
415	74	6.1	277	2	Q6MQ13	Q6mq13 bdellovibri	488	73	6.1	614	2	Q8MMA3	Q8mma3 drosophila
416	74	6.1	277	2	CAE78634	Cae78634 bdellovib	489	73	6.1	701	2	Q88XD1	Q88xd1 lactobacill
417	74	6.1	292	2	Q8CSR0	Q8csr0 staphylococ	490	73	6.1	747	1	AMD1_HUMAN	P23109 homo sapien
418	74	6.1	319	1	Y084_LISMO	Q8y7a4 listeria mo	491	73	6.1	825	2	Q7SHP1	Q7shp1 neurospora
419	74	6.1	319	1	Y221_LISIN	Q92bx1 listeria in	492	73	6.1	825	2	Q6PYB6	Q6pyb6 lemur catta
420	74	6.1	319	2	Q7IZT6	Q7izt6 listeria mo	493	73	6.1	825	2	AA592243	Aas92243 lemur cat
421	74	6.1	319	2	AA704178	Aat04178 listeria	494	73	6.1	847	2	Q8BFR2	Q8bfr2 m mus muscu
422	74	6.1	396	2	P74403	P74403 synchocyst	495	73	6.1	847	2	Q8C4T3	Q8c4t3 mus musculu
423	74	6.1	396	2	Q74403	Aar00595 oryza sat	496	73	6.1	1085	2	Q876N1	Q876n1 aspergillus
424	74	6.1	396	2	AA800595	Aar00595 oryza sat	497	73	6.1	1452	2	Q8UYV8	Q8uyv8 strawberry
425	74	6.1	398	2	Q7UQNS	Q7uqn5 rhodopirell	498	73	6.1	1711	1	PTPV_RAT	Q64612 rattus norv
426	74	6.1	414	2	Q8Z710	Q8z710 salmonella	499	72.5	6.0	403	2	Q6PKH7	Q6pkh7 homo sapien
427	74	6.1	414	2	Q8ZQ00	Q8zq00 salmonella	500	72.5	6.0	403	2	Q6VVE2	Q6vve2 oryza sativ
428	74	6.1	444	2	Q8BK47	Q8bk47 mus musculu	501	72.5	6.0	403	2	AAH00650	Aah00650 homo sapi
429	74	6.1	533	2	Q73L68	Q73l68 treponema d	502	72.5	6.0	403	2	BAC84534	Bac84534 oryza sat
430	74	6.1	533	2	AA512410	Aas12410 treponema	503	72.5	6.0	407	2	Q6MWO6	Q6mw06 neurospora
431	74	6.1	558	2	Q7QUO5	Q7qud5 giardia lam	504	72.5	6.0	407	2	CAE76145	Cae76145 neurospor
432	74	6.1	637	2	Q94H33	Q94h33 oryza sativ	505	72.5	6.0	431	2	Q7RXV8	Q7rxv8 neurospora
433	74	6.1	653	2	Q75HM8	Q75hm8 oryza sativ	506	72.5	6.0	447	1	FBX9_HUMAN	Q9ukx7 homo sapien
434	74	6.1	653	2	AA87358	Aar87358 oryza sat	507	72.5	6.0	513	2	Q6RJT3	Q6rjt3 candida gla
435	74	6.1	850	2	Q7QJY5	Q7qjy5 anopheles g	508	72.5	6.0	547	2	Q9NT57	Q9nt57 homo sapien
436	73.5	6.1	148	2	Q739V7	Q739v7 bacillus ce	509	72.5	6.0	644	2	Q64042	Q64042 bacterioph
437	73.5	6.1	214	2	AA540954	Aas40954 bacillus	510	72.5	6.0	644	2	Q31980	Q31980 bacillus su
438	73.5	6.1	214	2	Q73YB4	Q73y74 mycobacteri	511	72.5	6.0	667	2	Q7NWK2	Q7nwk2 chromobacte
439	73.5	6.1	214	2	AA504208	Aas04208 mycobacte	512	72.5	6.0	1062	2	Q96X97	Q96x97 sulfolobus
440	73.5	6.1	240	1	GTOL_MOUSE	Aas04208 mycobacte	513	72.5	6.0	1211	1	PKP4_HUMAN	Q95x69 homo sapien
441	73.5	6.1	240	2	BAC25667	Bac25667 mus muscu	514	72.5	6.0	1317	2	Q5FTQ6	Q5ftq6 candida gla
442	73.5	6.1	249	2	Q93P96	Q93p96 microscilla	515	72.5	6.0	1414	2	Q7S131	Q7s131 neurospora
443	73.5	6.1	260	2	Q73SP3	Q73sp3 mycobacteri	516	72.5	6.0	2727	2	Q6NR00	Q6nr00 drosophila
444	73.5	6.1	260	2	AA506580	Aas06580 mycobacte	517	72.5	6.0	2727	2	Q9VL06	Q9vl06 drosophila
445	73.5	6.1	287	2	Q6CG89	Q6cge9 yarrowia li	518	72.5	6.0	2727	2	AAQ23602	Aaq23602 drosophila
446	73.5	6.1	313	2	Q7U8G9	Q7u8g9 synchococc	519	72	6.0	169	2	Q88ZG3	Q88zg3 lactobacill
447	73.5	6.1	366	2	Q7I1B9	Q7i1b9 pseudomonas	520	72	6.0	171	1	VY03_BRAJA	Q89qml bradyrhizob
448	73.5	6.1	380	2	Q6WSB8	Q6wsb8 amycolatops	521	72	6.0	186	2	Q9JTL1	Q9jtl1 neisseria m
449	73.5	6.1	380	2	AAQ21336	Aaq21336 amycolato	522	72	6.0	191	1	EXOI_RHIME	Q52928 thizobium m
450	73.5	6.1	386	2	Q6DDJ2	Q6ddj2 xenopus lae	523	72	6.0	265	1	HL_PEA	P08283 pisum sativ
451	73.5	6.1	410	2	Q9CZK0	Q9czk0 mus musculu	524	72	6.0	276	2	Q9MCA9	Q9mca9 bacterioph
452	73.5	6.1	426	2	Q832V7	Q832v7 enterococcu	525	72	6.0	276	2	P73137	P73137 synchocyst
453	73.5	6.1	465	2	Q6C059	Q6c059 yarrowia li	526	72	6.0	303	2	Q9M5J0	Q9m5j0 phascolus a
454	73.5	6.1	503	1	SHS1_HUMAN	P78324 h protein-t	527	72	6.0	340	2	Q7ZY42	Q7zy42 xenopus lae
455	73.5	6.1	593	2	Q8S2E7	Q8s2e7 oryza sativ	528	72	6.0	363	2	Q9HX38	Q9hx38 pseudomonas
456	73.5	6.1	607	2	Q7R3S2	Q7r3s2 giardia lam	529	72	6.0	392	2	Q8CQZ3	Q8cqz3 kluyveromyc
457	73.5	6.1	615	2	Q6GNK4	Q6gnk4 xenopus lae	530	72	6.0	407	2	Q9BHB3	Q9bhb3 mus musculu
458	73.5	6.1	635	2	Q96LR8	Q96lr8 homo sapien	531	72	6.0	428	2	Q9RYM5	Q9rym5 deinooccus
459	73.5	6.1	684	2	Q8EK21	Q8ek21 shewanella	532	72	6.0	509	2	Q95BL8	Q95bl8 cimicifuga
460	73.5	6.1	846	2	Q86W98	Q86w98 homo sapien	533	72	6.0	564	2	Q7S022	Q7s022 neurospora
461	73.5	6.1	882	2	Q6NSL7	Q6ns17 rhodopseudo	534	72	6.0	600	2	Q7S022	Q7s022 neurospora
462	73.5	6.1	882	2	CAE28398	Cae28398 rhodopseu	535	72	6.0	602	1	TX15_MOUSE	Q91s72 arabidopsis
463	73.5	6.1	1044	2	Q94173	Q94173 pneumocysti	536	72	6.0	626	1	PFOC_LYCES	Q70306 mus musculu
464	73.5	6.1	1102	2	Q8IV23	Q8iv23 homo sapien	537	72	6.0	630	1	PFOA_LYCES	Q08305 lycopersico
465	73.5	6.1	1102	2	AAQ96873	Aaq96873 homo sapi	538	72	6.0	668	2	Q6NUM6	Q6num6 homo sapien
466	73.5	6.1	1372	2	Q9HAW1	Q9haw1 homo sapien	539	72	6.0	668	2	AAH68520	Aah68520 homo sapi
467	73.5	6.1	1388	2	Q9HAW2	Q9haw2 homo sapien	540	72	6.0	691	2	Q87Q21	Q87q21 vibrio para
468	73.5	6.1	2187	2	Q9H197	Q9h197 homo sapien	541	72	6.0	733	2	Q7PWR1	Q7pwr1 anopheles g
469	73.5	6.1	2254	2	Q9HCY0	Q9hcy0 homo sapien	542	72	6.0				

543	72	6.0	765	2	Q9UYV1	Q9UYV1 pneumocysti	616	70.5	5.9	158	2	Q9F9L6	Q9F9L6 methanotrop
544	72	6.0	836	2	Q8GST0	Q8GST0 oryza sativ	617	70.5	5.9	184	2	Q96CG3	Q96CG3 homo sapien
545	72	6.0	984	1	SECA_AQUAE	Q67718 aquifex ao	618	70.5	5.9	237	2	O58524	O58524 pyrococcus
546	72	6.0	1051	2	Q6PCR8	Q6PCR8 mus musculu	619	70.5	5.9	253	2	Q7NKU9	Q7NKU9 gloeobacter
547	72	6.0	1051	2	AAH59194	Aah59194 mus muscu	620	70.5	5.9	280	2	Q9DLC9	Q9DLC9 n mus muscu
548	72	6.0	1085	2	Q81117	Q81117 mus musculu	621	70.5	5.9	291	2	Q82SF4	Q82SF4 nitrosomona
549	72	6.0	1104	1	SYV_YEAST	P07806 saccharomyc	622	70.5	5.9	301	2	Q6DAW7	Q6DAW7 erwinia car
550	72	6.0	1115	2	Q90ZM5	Q90ZM5 gallus gall	623	70.5	5.9	301	2	Q91RL8	Q91RL8 rabies viru
551	72	6.0	1129	2	Q8PTJ5	Q8PTJ5 methanosarc	624	70.5	5.9	338	2	Q88IC3	Q88IC3 pseudomonas
552	72	6.0	1482	2	Q6ZQF9	Q6ZQF9 mus musculu	625	70.5	5.9	370	2	Q88FE7	Q88FE7 vibrio vuln
553	72	6.0	1492	2	BAC97905	Bac97905 mus muscu	626	70.5	5.9	374	2	Q9LLQ7	Q9LLQ7 vigne ungu
554	72	6.0	1674	2	Q86BF4	Q86BF4 drosophila	627	70.5	5.9	390	2	Q8UWM1	Q8UWM1 brachydanio
555	72	6.0	1908	2	Q9V8K9	Q9V8K9 drosophila	628	70.5	5.9	392	2	Q6MHE3	Q6MHE3 bdellovibri
556	72	6.0	2087	2	Q86RF6	Q86RF6 drosophila	629	70.5	5.9	392	2	CAE80984	CAE80984 bdellovib
557	71.5	5.9	184	2	Q9VKI7	Q7VKI7 haemophilus	630	70.5	5.9	398	2	P77842	P77842 chloroflexu
558	71.5	5.9	194	2	Q7VKI7	Q7VKI7 haemophilus	631	70.5	5.9	423	1	TX2 CAEEL	TX2 CAEEL caenorhabdi
559	71.5	5.9	258	2	Q92ZG5	Q92ZG5 rhizobium m	632	70.5	5.9	436	2	Q8TU02	Q8TU02 caenorhabdi
560	71.5	5.9	289	2	Q72MV9	Q72MV9 leptospira	633	70.5	5.9	460	2	Q9FG85	Q9FG85 arabidopsis
561	71.5	5.9	289	2	AA571629	AA571629 leptospir	634	70.5	5.9	507	2	Q9LSJ3	Q9LSJ3 arabidopsis
562	71.5	5.9	301	2	Q8EZJ8	Q8EZJ8 leptospira	635	70.5	5.9	525	1	NCAP_RINDR	NCAP_RINDR rinderpest
563	71.5	5.9	335	2	Q7NZK1	Q7NZK1 chromobacte	636	70.5	5.9	525	2	Q86381	Q86381 rinderpest
564	71.5	5.9	334	2	Q9PHW0	Q9PHW0 campylobact	637	70.5	5.9	532	1	CAX2 ARATH	CAX2 ARATH arabidopsis
565	71.5	5.9	342	2	Q8RFR9	Q8RFR9 fusobacteri	638	70.5	5.9	532	2	AAW72010	AAW72010 arabidops
566	71.5	5.9	370	2	Q7MN01	Q7MN01 vibrio vuln	639	70.5	5.9	532	2	AAQ56828	AAQ56828 arabidops
567	71.5	5.9	392	2	Q9K688	Q9K688 bacillus ha	640	70.5	5.9	606	2	Q75IR7	Q75IR7 oryza sativ
568	71.5	5.9	421	2	Q33935	Q33935 saccharopol	641	70.5	5.9	606	2	AAT07655	AAT07655 oryza sat
569	71.5	5.9	421	2	O54224	O54224 saccharopol	642	70.5	5.9	665	1	GAK3 HUMAN	GAK3 HUMAN homo sapien
570	71.5	5.9	462	2	Q93PB4	Q93PB4 microscilla	643	70.5	5.9	668	2	Q6BWA2	Q6BWA2 debaryomyce
571	71.5	5.9	486	2	Q9SGQ0	Q9SGQ0 arabidopsis	644	70.5	5.9	703	2	Q7N9Q5	Q7N9Q5 photorhabdu
572	71.5	5.9	486	2	BAD17857	BAD17857 arabidops	645	70.5	5.9	710	1	FOXA YEREN	FOXA YEREN yersinia en
573	71.5	5.9	513	2	Q6BTO8	Q6BTO8 debaryomyce	646	70.5	5.9	792	2	Q7XIG8	Q7XIG8 oryza sativ
574	71.5	5.9	588	2	Q9PVX5	Q9PVX5 cynops pyr	647	70.5	5.9	807	2	Q9XFX7	Q9XFX7 craterostig
575	71.5	5.9	592	2	Q8THB6	Q8THB6 methanosarc	648	70.5	5.9	830	1	FAR1 YEAST	FAR1 YEAST saccharomyc
576	71.5	5.9	632	2	Q8D486	Q8D486 vibrio vuln	649	70.5	5.9	917	2	Q89KU0	Q89KU0 bradyrhizob
577	71.5	5.9	649	2	Q9SZK3	Q9SZK3 arabidopsis	650	70.5	5.9	937	2	O6LLQ4	O6LLQ4 photobacter
578	71.5	5.9	666	2	Q7S0B3	Q7S0B3 neurospora	651	70.5	5.9	937	2	CAG21774	CAG21774 photobact
579	71.5	5.9	692	2	Q89FD2	Q89FD2 bradyrhizob	652	70.5	5.9	1139	1	K196_HUMAN	K196_HUMAN homo sapien
580	71.5	5.9	712	1	SYM_METAC	Q8TIU5 methanosarc	653	70.5	5.9	1159	1	K196_MOUSE	K196_MOUSE mus musculu
581	71.5	5.9	725	2	Q9JW26	Q9JW26 neisseria m	654	70.5	5.9	1298	2	Q6LNT1	Q6LNT1 photobacter
582	71.5	5.9	774	1	FECA_ECOLI	P13036 escherichia	655	70.5	5.9	1298	2	CAG21045	CAG21045 photobact
583	71.5	5.9	873	2	Q7ZAH0	Q7ZAH0 acidiana b	656	70.5	5.9	1340	2	Q8PEP6	Q8PEP6 xanthomonas
584	71.5	5.9	1047	2	Q8VYK0	Q8VYK0 anabaena sp	657	70.5	5.9	1465	1	YH85 SCHPO	YH85 SCHPO schizosacch
585	71.5	5.9	1729	2	Q7VVC2	Q7VVC2 bordetella	658	70.5	5.9	1574	2	Q7Y5J5	Q7Y5J5 xanthomonas
586	71	5.9	158	2	Q9APT0	Q9APT0 uncultured	659	70.5	5.9	1734	2	Q8MNL9	Q8MNL9 dictyosteli
587	71	5.9	171	2	Q6GAU6	Q6GAU6 staphylococ	660	70.5	5.9	1734	2	AAH34313	AAH34313 dictyoste
588	71	5.9	171	2	Q8NXA4	Q8NXA4 staphylococ	661	70.5	5.9	3914	2	Q70DK0	Q70DK0 bovine vira
589	71	5.9	189	2	Q8Y2K0	Q8Y2K0 ralstonia s	662	70.5	5.9	3914	2	CAE51342	CAE51342 bovine vi
590	71	5.9	238	2	Q6P3D6	Q6P3D6 mus musculu	663	70	5.8	171	2	Q6GIA7	Q6GIA7 staphylococ
591	71	5.9	238	2	AAH64039	AAH64039 mus muscu	664	70	5.8	191	2	Q753H6	Q753H6 ashbya goss
592	71	5.9	249	2	Q7Q8W7	Q7Q8W7 anopheles g	665	70	5.8	191	2	AA553707	AA553707 ashbya go
593	71	5.9	277	2	Q924V3	Q924V3 cricetus	666	70	5.8	215	2	Q6SJP8	Q6SJP8 brachydanio
594	71	5.9	299	2	Q9DGB0	Q9DGB0 xenopus lae	667	70	5.8	215	2	AAH20841	AAH20841 brachydan
595	71	5.9	316	2	Q837T2	Q837T2 enterococcu	668	70	5.8	257	2	Q8AVH2	Q8AVH2 pleurodeles
596	71	5.9	329	2	Q8NTR4	Q8NTR4 neurospora	669	70	5.8	322	2	Q8SQ26	Q8SQ26 sus scrofa
597	71	5.9	354	2	Q9D2D9	Q9D2D9 mus musculu	670	70	5.8	327	2	Q87W14	Q87W14 pseudomonas
598	71	5.9	638	2	Q6KAU0	Q6KAU0 mus musculu	671	70	5.8	332	2	Q88DN7	Q88DN7 pseudomonas
599	71	5.9	638	2	BAD21367	BAD21367 mus muscu	672	70	5.8	347	2	Q7WAY1	Q7WAY1 bordetella
600	71	5.9	659	1	GLGX_HAEIN	P45178 haemophilus	673	70	5.8	347	2	Q7WME5	Q7WME5 bordetella
601	71	5.9	833	1	CAPA_YERPE	P26949 yersinia pe	674	70	5.8	354	2	Q8IXV7	Q8IXV7 homo sapien
602	71	5.9	833	2	AAH30872	AAH30872 yersinia	675	70	5.8	354	2	AAH98754	AAH98754 homo sapi
603	71	5.9	833	2	AAH30877	AAH30877 yersinia	676	70	5.8	365	2	Q7VY98	Q7VY98 bordetella
604	71	5.9	833	2	AAH30880	AAH30880 yersinia	677	70	5.8	368	2	Q6F0V2	Q6F0V2 brachydanio
605	71	5.9	860	2	Q9NDT9	Q9NDT9 balanus amp	678	70	5.8	368	2	AAH65436	AAH65436 brachydan
606	71	5.9	989	2	Q7UVE2	Q7UVE2 rhodopirell	679	70	5.8	408	2	Q8N2K8	Q8N2K8 homo sapien
607	71	5.9	993	2	Q6PIF9	Q6PIF9 mus musculu	680	70	5.8	463	2	Q8T4S4	Q8T4S4 aedes aegyp
608	71	5.9	993	2	AAH65093	AAH65093 mus muscu	681	70	5.8	466	1	ACM2_CHICK	ACM2_CHICK gallus gall
609	71	5.9	1004	1	SLPO_BACBR	P09333 bacillus-br	682	70	5.8	469	1	Y0J8_CAEEL	Y0J8_CAEEL caenorhabdi
610	71	5.9	1048	2	Q7TNY8	Q7TNY8 mus musculu	683	70	5.8	474	2	Q89Y07	Q89Y07 bradyrhizob
611	71	5.9	1051	2	Q91XT4	Q91XT4 mus musculu	684	70	5.8	485	2	Q41832	Q41832 zea mays (m
612	71	5.9	1498	2	Q9Y4F5	Q9Y4F5 homo sapien	685	70	5.8	518	2	Q88G73	Q88G73 pseudomonas
613	71	5.9	1944	1	CHD3_HUMAN	Q12873 homo sapien	686	70	5.8	622	2	Q9FG16	Q9FG16 arabidopsis
614	71	5.9	2000	2	Q9Y4I0	Q9Y4I0 homo sapien	687	70	5.8	637	2	Q6DV10	Q6DV10 gekko japon
615	70.5	5.9	144	1	RS1A_SCHPO	O14112 schizosacch	688	70	5.8	641	2	Q9K543	Q9K543 vibrio chol

Q9F9L6	methanotrop
Q96CG3	homo sapien
O58524	pyrococcus
Q7NKU9	gloeobacter
Q9DLC9	n mus muscu
Q82SF4	nitrosomona
Q6DAW7	erwinia car
Q91RL8	rabies viru
Q88IC3	pseudomonas
Q88FE7	vibrio vuln
Q9LLQ7	vigne ungu
Q8UWM1	brachydanio
Q6MHE3	bdellovibri
CAE80984	bdellovib
P77842	chloroflexu
TX2 CAEEL	caenorhabdi
Q8TU02	caenorhabdi
Q9FG85	arabidopsis
Q9LSJ3	arabidopsis
NCAP_RINDR	rinderpest
Q86381	rinderpest
CAX2 ARATH	arabidopsis
AAW72010	arabidops
AAQ56828	arabidops
Q75IR7	oryza sativ
AAT07655	oryza sat
GAK3 HUMAN	homo sapien
Q6BWA2	debaromyce
Q7N9Q5	photorhabdu
FOXA YEREN	yersinia en
Q7XIG8	oryza sativ
Q9XFX7	craterostig
P21268	saccharomyc
Q89KU0	bradyrhizob
O6LLQ4	photobacter
CAG21774	photobact
Q12768	homo sapien
Q8CZ67	mus musculu
O6LNT1	photobacter
CAG21045	photobact
Q8PEP6	xanthomonas
Q9P5N0	schizosacch
Q7Y5J5	xanthomonas
Q8MNL9	dictyosteli
AAH34313	dictyoste
Q70DK0	bovine vira
CAE51342	bovine vi
Q6GIA7	staphylococ
Q753H6	ashbya goss
AA553707	ashbya go
Q6SJP8	brachydanio
AAH20841	brachydan
Q8AVH2	pleurodeles
Q8SQ26	sus scrofa
Q87W14	pseudomonas
Q88DN7	pseudomonas
Q7WAY1	bordetella
Q7WME5	bordetella
Q8IXV7	homo sapien
AAH98754	homo sapi
Q7VY98	bordetella
Q6F0V2	brachydanio
AAH65436	brachydan
Q8N2K8	homo sapien
Q8T4S4	aedes aegyp
ACM2_CHICK	gallus gall
Y0J8_CAEEL	caenorhabdi
Q89Y07	bradyrhizob
Q41832	zea mays (m
Q88G73	pseudomonas
Q9FG16	arabidopsis
Q6DV10	gekko japon
Q9K543	vibrio chol

689	70	5.8	703	2	O6BK2	O6bvk2 debaryomyce	762	69.5	5.8	1073	1	ACA9 ARATH	Q9lu41 arabidopsis
690	70	5.8	721	2	O6NVQ6	O6nvq6 xenopus tro	763	69.5	5.8	1140	2	Q9P3N7	Q9p3n7 neurospora
691	70	5.8	721	2	AAH67949	Aah67949 xenopus t	764	69.5	5.8	1250	2	Q82RX1	Q82rx1 streptomyce
692	70	5.8	743	2	O6FF05	O6ff05 acinetobact	765	69.5	5.8	1284	2	Q7RUY5	Q7ruy5 neurospora
693	70	5.8	784	2	O9HXB2	O9hxb2 pseudomonas	766	69.5	5.8	1456	2	Q8NJS1	Q8njs1 leptosphaer
694	70	5.8	801	2	O6FH33	O6fh33 candida gla	767	69.5	5.8	1550	2	Q6MW89	Q6mw89 oryza sativ
695	70	5.8	809	2	O7SRF1	O7srf1 neurospora	768	69.5	5.8	1550	2	CAE76056	CaE76056 oryza sat
696	70	5.8	813	2	O8WIB2	O8wb2 papaver som	769	69.5	5.8	1597	2	Q960M3	Q960m3 drosophila
697	70	5.8	813	2	AAH48261	Aah48261 papaver s	770	69.5	5.8	1730	2	Q6FJN8	Q6fjn8 candida gla
698	70	5.8	813	2	AAH48263	Aah48263 papaver s	771	69.5	5.8	1984	2	Q6QJVA	Q6qjva viral hemor
699	70	5.8	836	2	Q8N394	Q8n394 homo sapien	772	69.5	5.8	2029	1	LAR DROME	L16621 drosophila
700	70	5.8	874	2	O8JIS6	O8jis6 brachydanio	773	69.5	5.8	2029	2	Q9VIS8	Q9vis8 drosophila
701	70	5.8	874	2	O8JIS6	O8jis6 brachydanio	774	69.5	5.8	2270	2	Q9NSJ3	Q9nsj3 homo sapien
702	70	5.8	893	2	O6S119	O6s119 uncultured	775	69.5	5.8	3209	2	Q9UIM0	Q9uim0 homo sapien
703	70	5.8	893	2	AAH37453	Aah37453 unculture	776	69.5	5.8	4363	2	Q709C4	Q709c4 homo sapien
704	70	5.8	983	2	O8GZ04	O8gz04 arabidopsis	777	69.5	5.8	4363	2	CAE75587	CaE75587 homo sapi
705	70	5.8	985	2	O8VY05	O8vy05 arabidopsis	778	69.5	5.8	4388	2	Q709C5	Q709c5 homo sapien
706	70	5.8	1395	2	Q35059	Q35059 marchantia	779	69.5	5.8	4388	2	CAE75586	CaE75586 homo sapi
707	70	5.8	2137	2	O15021	O15021 homo sapien	780	69	5.7	106	2	O27418	O27418 methanobact
708	70	5.8	2860	2	O8I640	O8i640 plasmodium	781	69	5.7	190	2	Q9SHP3	Q9shp3 arabidopsis
709	70	5.8	6797	2	Q9X993	Q9x993 streptomyce	782	69	5.7	222	2	Q8BRP4	Q8brp4 mus musculu
710	69.5	5.8	204	2	Q87C69	Q87c69 xyliella fas	783	69	5.7	235	2	Q9FGU9	Q9fgu9 xyliella fas
711	69.5	5.8	215	2	Q716N9	Q716n9 mycobacteri	784	69	5.7	236	2	Q6DEF7	Q6def7 brachydanio
712	69.5	5.8	215	2	AAQ12113	Aaq12113 mycobacte	785	69	5.7	257	2	O8ASQ7	O8asq7 bacteroides
713	69.5	5.8	255	1	Y439 PYRHO	O58186 pyrococcus	786	69	5.7	297	2	O8YQJ8	O8yqj8 anabaena sp
714	69.5	5.8	259	2	O8E564	O8e64 schistosoma	787	69	5.7	313	2	O9XS24	O9xs24 ateles fusc
715	69.5	5.8	263	2	O8MIC5	O8mic5 ovis aries	788	69	5.7	320	2	O8XK96	O8xk96 clostridium
716	69.5	5.8	268	2	Q74EV9	Q74ev9 geobacter s	789	69	5.7	365	2	Q9FW23	Q9fw23 gallus gall
717	69.5	5.8	268	2	AAH34180	Aah34180 geobacter	790	69	5.7	368	2	Q7ZT37	Q7zt37 brachydanio
718	69.5	5.8	277	2	O8FAX7	O8fax7 escherichia	791	69	5.7	378	2	Q9FHZ5	Q9fhz5 arabidopsis
719	69.5	5.8	291	2	O6LU44	O6lu44 photobacter	792	69	5.7	403	2	Q9P5S5	Q9p5s5 neurospora
720	69.5	5.8	291	2	CAG19181	Cag19181 photobact	793	69	5.7	415	1	L52 ADE02	P03262 human adeno
721	69.5	5.8	312	1	HEM3 VIEVU	O8dd85 vibrio vuln	794	69	5.7	415	2	O71EX5	Q71lx5 human adeno
722	69.5	5.8	312	2	Q7MQC7	Q7mqc7 vibrio vuln	795	69	5.7	415	2	Q7MG33	Q7m633 human adeno
723	69.5	5.8	327	2	Q7NEA1	Q7neal1 geobacter	796	69	5.7	415	2	AAQ10546	Aaq10546 human ade
724	69.5	5.8	336	1	VG27 BPMLS	Q05234 mycobacteri	797	69	5.7	416	2	Q8EEV4	Q8eev4 shewanella
725	69.5	5.8	346	1	AMBP MERUN	O62577 meriones un	798	69	5.7	424	2	Q8LBB2	Q8lbb2 arabidopsis
726	69.5	5.8	365	2	O87RP5	O87rp5 vibrio para	799	69	5.7	428	2	Q93F17	Q93f17 shigella fl
727	69.5	5.8	379	2	O9HGW1	O9hgw1 protomyces	800	69	5.7	463	2	O8T4S6	O8t4s6 aedes aegyp
728	69.5	5.8	389	2	Q9D828	Q9d828 mus musculu	801	69	5.7	493	2	Q71EP1	Q71ep1 betta pugna
729	69.5	5.8	391	2	Q75PR0	Q75pr0 physcomitre	802	69	5.7	493	2	AAQ08541	Aaq08541 betta pug
730	69.5	5.8	391	2	BAD12233	Badi2233 physcomit	803	69	5.7	506	1	SHS1 BOVIN	O4631 bos taurus
731	69.5	5.8	416	2	Q7XX65	O7xx65 oryza sativ	804	69	5.7	522	2	Q6D2I3	Q6d2i3 erwinia car
732	69.5	5.8	418	2	O88TV5	O88tv5 lactobacilli	805	69	5.7	527	1	ATRX RAT	P70486 rattus norv
733	69.5	5.8	420	2	O6W970	O6w970 tenebrio mo	806	69	5.7	539	2	Q9M2B8	Q9m2b8 arabidopsis
734	69.5	5.8	420	2	AAQ72749	Aaq72749 tenebrio	807	69	5.7	541	2	O7W5T4	Q7w5t4 bordetella
735	69.5	5.8	431	2	Q73V92	Q73v92 mycobacteri	808	69	5.7	544	2	Q7WDH4	Q7wdh4 bordetella
736	69.5	5.8	431	2	AAH05670	Aah05670 mycobacte	809	69	5.7	546	2	Q6UIQ5	Q6uiq5 esox masqui
737	69.5	5.8	456	2	Q9LZ15	Q9lzl5 arabidopsis	810	69	5.7	546	2	AAH27497	Aar27497 esox masq
738	69.5	5.8	462	2	Q92S06	Q92s06 rhizobium m	811	69	5.7	672	2	Q96NG3	Q96ng3 homo sapien
739	69.5	5.8	476	2	O8YU75	O8yu75 anabaena sp	812	69	5.7	674	2	O96SY5	Q96sy5 homo sapien
740	69.5	5.8	492	2	Q9ZSQ2	Q9zsq2 pisum sativ	813	69	5.7	686	1	IPL2 MOUSE	Q9ers6 mus musculu
741	69.5	5.8	499	2	Q7WU92	Q7wu92 thermotoga	814	69	5.7	701	2	Q9ASJ4	Q9asj4 oryza sativ
742	69.5	5.8	525	1	NCAP RINDU	P41359 rinderpest	815	69	5.7	724	2	Q6C9H6	Q6c9h6 yarrowia li
743	69.5	5.8	566	2	Q91N43	Q91n43 bovine vira	816	69	5.7	733	2	Q7SIG8	Q7sig8 desulfuroco
744	69.5	5.8	588	2	Q835N0	Q835n0 enterococcu	817	69	5.7	747	2	Q98TE7	Q98te7 carassius a
745	69.5	5.8	599	2	O41428	O41428 solanum tub	818	69	5.7	764	2	O8FJB3	Q8fjb3 escherichia
746	69.5	5.8	717	2	O6P3G5	O6p3g5 brachydanio	819	69	5.7	773	2	Q7SIG7	Q7sig7 desulfuroco
747	69.5	5.8	717	2	AAH63996	Aah63996 brachydan	820	69	5.7	780	2	Q7AG55	Q7ag55 escherichia
748	69.5	5.8	725	2	Q7V771	Q7vt71 bordetella	821	69	5.7	780	2	Q8XEA2	Q8xea2 escherichia
749	69.5	5.8	725	2	Q7W294	Q7wr24 bordetella	822	69	5.7	780	2	Q8XEA2	Q8xea2 papaver som
750	69.5	5.8	725	2	Q7WR61	Q7wr61 bordetella	823	69	5.7	813	2	Q8VWE9	Q8vwe9 papaver som
751	69.5	5.8	747	1	AMD1 RAT	P10759 rattus norv	824	69	5.7	813	2	AAH48262	Aal48262 papaver s
752	69.5	5.8	754	1	YCAI_ECOLI	P37443 escherichia	825	69	5.7	813	2	AAH48264	Aal48264 papaver s
753	69.5	5.8	793	1	AD28_MOUSE	Q9jln6 mus musculu	826	69	5.7	814	2	O8TB54	Q8tb54 homo sapien
754	69.5	5.8	811	2	O6PFE5	O6pf55 xenopus lae	827	69	5.7	815	2	O84NP7	Q84np7 oryza sativ
755	69.5	5.8	811	2	AAH57722	Aah57722 xenopus l	828	69	5.7	818	2	O8N4X5	Q8n4x5 homo sapien
756	69.5	5.8	840	2	Q9BPN3	Q9bpn3 caenorhabdi	829	69	5.7	831	2	Q8XX81	Q8xx81 raistonia s
757	69.5	5.8	841	2	Q7USV0	Q7usv0 rhodospirell	830	69	5.7	834	1	AG01 SCHPO	P74957 schizosacch
758	69.5	5.8	857	2	Q74H88	Q74h88 geobacter s	831	69	5.7	892	2	P91085	P91085 caenorhabdi
759	69.5	5.8	857	2	AAH33339	Aah33339 geobacter	832	69	5.7	921	2	O8SS27	Q8ss27 encephalito
760	69.5	5.8	910	1	DDHA_RHOSU	O8gpg4 rhodovulum	833	69	5.7	1100	2	O80WC9	Q80wc9 mus musculu
761	69.5	5.8	914	2	Q7QY57	Q7qy57 giardia lam	834	69	5.7	1112	2	Q8WZV2	Q8wzv2 neurospora

835	69	5.7	1693	2	Q9P655	Q9P655 neurospora	68.5	908	5.7	5379	2	Q9FDB3	Q9fdb3 pseudomonas
836	68.5	5.7	154	2	Q90Z14	Q90Z14 xenopus lae	68	909	5.6	153	2	Q8T601	Q8t601 schistosoma
837	68.5	5.7	157	1	HS11 DAUCA	P27396 daucus caro	68	910	5.6	183	2	Q8BPT5	Q8bpt5 mus musculus
838	68.5	5.7	164	2	Q88TD6	Q88td6 lactobacilli	68	911	5.6	191	2	Q73201	Q73201 mycobacteri
839	68.5	5.7	167	2	Q7NVY0	Q7nvY0 chromobacte	68	912	5.6	191	2	AA504119	AA504119 mycobacte
840	68.5	5.7	169	2	Q825J0	Q825j0 streptomyc	68	913	5.6	205	2	Q9IOX8	Q9iOx8 pseudomonas
841	68.5	5.7	175	1	COAG CARRO	P03997 carinosecor	68	914	5.6	224	1	MED2 MOUSE	Q9erx7 mus musculu
842	68.5	5.7	188	1	EFPL_XYLFT	Q87c43 xyliella fas	68	915	5.6	224	2	Q8CCX7	Q8ccx7 mus musculu
843	68.5	5.7	189	1	EFPL_XYLFA	Q9pbe1 xyliella fas	68	916	5.6	224	2	BAC36471	BAC36471 mus muscu
844	68.5	5.7	203	2	Q7P5G5	Q7p5G5 fusobacteri	68	917	5.6	229	2	Q48389	Q48389 klebsiella
845	68.5	5.7	203	2	Q8R182	Q8r182 fusobacteri	68	918	5.6	237	2	Q8C611	Q8c611 mus musculu
846	68.5	5.7	210	2	Q9VNN5	Q9vnn5 drosophila	68	919	5.6	253	2	Q8EXF6	Q8ekf6 shewanella
847	68.5	5.7	224	2	Q9RU88	Q9ru88 deinoxoccus	68	920	5.6	277	2	Q924V2	Q924v2 cricetus
848	68.5	5.7	229	2	Q9HMR8	Q9hmr8 halobacteri	68	921	5.6	278	2	Q8L112	Q8l112 oryza sativ
849	68.5	5.7	276	2	Q23926	Q23926 dictyosteli	68	922	5.6	290	2	Q6MDP3	Q6mdp3 parachlamyd
850	68.5	5.7	280	2	Q8CCX8	Q8ccx8 mus musculu	68	923	5.6	290	2	CAF223306	Caf223306 parachlam
851	68.5	5.7	298	2	Q8R257	Q8r257 mus musculu	68	924	5.6	303	2	Q829X2	Q829x2 streptomyc
852	68.5	5.7	304	2	Q92QY4	Q92qy4 rhizobium m	68	925	5.6	308	2	Q8T4S5	Q8t4s5 aedes aegyp
853	68.5	5.7	322	2	Q6F9Y0	Q6f9Y0 acinetobact	68	926	5.6	324	2	Q8Q0F5	Q8q0F5 methanosarc
854	68.5	5.7	335	1	YD59 SCHPO	Q10312 schizosacch	68	927	5.6	332	2	Q71UV2	Q71uv2 homo sapien
855	68.5	5.7	351	2	Q70BFL0	Q70p10 macaca mula	68	928	5.6	332	2	O77644	O77644 pan troglod
856	68.5	5.7	351	2	CAD89646	Cad89646 macaca mu	68	929	5.6	332	2	AAC61679	Aac61679 homo sapi
857	68.5	5.7	354	2	Q91N46	Q91n46 bovine vira	68	930	5.6	340	2	Q87VY0	Q87vy0 pseudomonas
858	68.5	5.7	355	2	Q74245	Q74245 ashbya goss	68	931	5.6	341	2	Q7XBA6	Q7xra6 oryza sativ
859	68.5	5.7	355	2	AA54851	AA54851 ashbya go	68	932	5.6	342	2	Q7P6P3	Q7p6P3 fusobacteri
860	68.5	5.7	374	1	CARA_XYLFA	Q9pec2 xyliella fas	68	933	5.6	352	2	Q7U5C6	Q7u5C6 synechococc
861	68.5	5.7	405	2	Q8TLB6	Q8tlb6 methanosarc	68	934	5.6	371	2	Q6GMK4	Q6gmK4 brachydanio
862	68.5	5.7	406	2	Q94147	Q94147 oryza sativ	68	935	5.6	378	2	Q8L8L1	Q8l8L1 arabidopsis
863	68.5	5.7	419	2	Q6W978	Q6w978 diplopoda s	68	936	5.6	380	2	Q8IR27	Q8ir27 drosophila
864	68.5	5.7	419	2	Q8RR24	Q8rr24 streptomyc	68	937	5.6	391	2	Q9S2B3	Q9s2B3 streptomyc
865	68.5	5.7	419	2	AAQ72741	AAq72741 diplopoda	68	938	5.6	400	2	Q86TK5	Q86tK5 homo sapien
866	68.5	5.7	420	2	Q6W971	Q6w971 harmonia ax	68	939	5.6	403	2	O23109	O23109 arabidopsis
867	68.5	5.7	420	2	AAQ72748	AAq72748 harmonia	68	940	5.6	414	2	Q6PGN5	Q6pgN5 homo sapien
868	68.5	5.7	425	2	Q8S9B0	Q8s9B0 brassica ca	68	941	5.6	414	2	AAH56915	Aah56915 homo sapi
869	68.5	5.7	446	2	Q9ME7	Q9me7 mus musculu	68	942	5.6	415	1	L52 ADE05	P04496 human adeno
870	68.5	5.7	470	2	Q8W1A1	Q8w1A1 glycine max	68	943	5.6	415	2	Q7M5Z2	Q7m5Z2 human adeno
871	68.5	5.7	471	2	Q35162	Q35162 rattus norv	68	944	5.6	422	2	Q74H55	Q74h55 geobacter s
872	68.5	5.7	471	2	Q6IRE1	Q6ire1 rattus norv	68	945	5.6	422	2	AAH33372	AAh33372 geobacter
873	68.5	5.7	471	2	AAH70954	AAh70954 rattus no	68	946	5.6	424	2	Q9S7W6	Q9s7W6 arabidopsis
874	68.5	5.7	502	1	RM02 ORYSA	P92812 oryza sativ	68	947	5.6	440	2	Q7V3Y1	Q7v3Y1 prochloroco
875	68.5	5.7	502	1	Q8HCN7	Q8hcn7 oryza sativ	68	948	5.6	442	2	Q9SDP3	Q9sdP3 allium cepa
876	68.5	5.7	508	2	Q6NH93	Q6nh93 corynebacte	68	949	5.6	448	2	Q6C4G6	Q6c4G6 yarrowia li
877	68.5	5.7	508	2	CAE49776	CAe49776 corynebac	68	950	5.6	449	2	Q9SKN9	Q9sKn9 macaca fasc
878	68.5	5.7	573	2	Q7MQP8	Q7mqp8 wolfinella s	68	951	5.6	449	2	Q9SK03	Q9sk03 arabidopsis
879	68.5	5.7	573	2	Q994E5	Q994e5 porcine ade	68	952	5.6	455	2	Q9N134	Q9n134 coryctolagus
880	68.5	5.7	575	2	Q8MZS4	Q8mzS4 physarum po	68	953	5.6	456	2	Q93CS1	Q93cs1 shigella bo
881	68.5	5.7	671	2	Q7XHY3	Q7xhy3 oryza sativ	68	954	5.6	459	2	O50578	O50578 pseudomonas
882	68.5	5.7	695	2	Q9SU22	Q9su22 arabidopsis	68	955	5.6	462	2	Q8T4S3	Q8t4S3 aedes aegyp
883	68.5	5.7	706	2	O59058	O59058 pyrococcus	68	956	5.6	463	2	Q8T4S1	Q8t4S1 aedes aegyp
884	68.5	5.7	754	2	Q8Z802	Q8z802 salmonella	68	957	5.6	463	2	Q8T4S2	Q8t4S2 aedes aegyp
885	68.5	5.7	755	2	Q7VBL4	Q7vbl4 prochloroco	68	958	5.6	466	2	Q7SXF5	Q7sxf5 brachydanio
886	68.5	5.7	761	2	Q7RYW3	Q7ryw3 neurospora	68	959	5.6	475	1	L1PL HUMAN	P06858 homo sapien
887	68.5	5.7	812	2	Q7RWE4	Q7rwe4 neurospora	68	960	5.6	475	1	L1PL HUMAN	P49060 papio anubi
888	68.5	5.7	827	2	Q7UPJ6	Q7upj6 rhodopirell	68	961	5.6	475	2	Q61A70	Q61aV0 homo sapien
889	68.5	5.7	860	2	Q9ZWN6	Q9znw6 brassica ca	68	962	5.6	475	2	CAG33335	Cag33335 homo sapi
890	68.5	5.7	873	2	Q9LS59	Q9lS59 arabidopsis	68	963	5.6	486	2	Q8XUI0	Q8xui0 ralstonia s
891	68.5	5.7	882	2	Q9HYV3	Q9hyv3 pseudomonas	68	964	5.6	491	2	Q6T6W6	Q6t6W6 stokellia a
892	68.5	5.7	948	2	Q9U304	Q9u304 caenorhabdi	68	965	5.6	491	2	AAH92385	Aah92385 stokellia
893	68.5	5.7	980	2	Q8ACJ1	Q8a3j1 bacteroides	68	966	5.6	506	2	Q8TWB5	Q8twb5 methanopyru
894	68.5	5.7	1050	2	Q8CC14	Q8cc14 mus musculu	68	967	5.6	535	2	Q8T125	Q8t125 arabidopsis
895	68.5	5.7	1059	2	Q9NBB9	Q9nbb9 trypanosoma	68	968	5.6	538	2	Q8LKN1	Q8lkn1 arachis hyp
896	68.5	5.7	1096	2	Q7EZ84	Q7ez84 oryza sativ	68	969	5.6	551	2	Q6EZ45	Q6ez45 neurospora
897	68.5	5.7	1096	2	BAD09972	Bad09972 oryza sat	68	970	5.6	576	2	Q7S4G2	Q7s4G2 burkholderi
898	68.5	5.7	1096	2	BAD09994	Bad09994 oryza sat	68	971	5.6	585	2	Q7LCY6	Q7lcy6 homo sapien
899	68.5	5.7	1125	2	Q93TH9	Q93th9 bacteroides	68	972	5.6	585	2	Q9UH65	Q9uh65 homo sapien
900	68.5	5.7	1181	2	Q6MY2	Q6my2 homo sapien	68	973	5.6	585	2	Q88443	Q88443 mus musculu
901	68.5	5.7	1181	2	CAE45895	CAe45895 homo sapi	68	974	5.6	585	2	Q6F1D0	Q6fd0 mus musculu
902	68.5	5.7	1261	2	Q6RY08	Q6ry08 asterina ml	68	975	5.6	585	2	AAH65136	Aah65136 mus muscu
903	68.5	5.7	1261	2	AAH85355	Aar85355 asterina	68	976	5.6	603	2	Q7S135	Q7s135 homo sapien
904	68.5	5.7	1609	2	Q4XTW1	Q4xtw1 oryza sativ	68	977	5.6	670	2	Q9ER33	Q9er33 rattus norv
905	68.5	5.7	2199	2	Q6DNE5	Q6dne5 lyncbysa maj	68	978	5.6	732	2	Q74LC3	Q74lc3 lactobacilli
906	68.5	5.7	3869	2	Q7WRN5	Q7wrn5 anabaena ci	68	979	5.6	732	2	AA508244	Aa508244 lactobaci
907	68.5	5.7	4307	2	Q19319	Q19319 caenorhabdi	68	980	5.6	762	2	Q9VXQ6	Q9vxq6 drosophila

981	68	5.6	848	2	Q83HG8	Q83hg8 tropheryma	1054	67.5	5.6	513	2	Q6PFL3	Q6pfl3 brachydanio
982	68	5.6	870	2	Q7AM69	Q74m69 nanoarchaeu	1055	67.5	5.6	513	2	AAH57505	Aah57505 brachydan
983	68	5.6	870	2	AAK39345	Aar39345 nanoarcha	1056	67.5	5.6	516	2	Q222Y1	Q22y1 rhizobium m
984	68	5.6	876	2	Q83GT6	Q83gt6 tropheryma	1057	67.5	5.6	532	1	INV4 YEAST	P10596 saccharomyc
985	68	5.6	893	2	Q8KPV2	Q8kpv2 synechococc	1058	67.5	5.6	550	2	Q7AGJ9	Q7agj9 escherichia
986	68	5.6	1021	2	O06342	O06342 mycobacteri	1059	67.5	5.6	550	2	Q8X999	Q8x999 escherichia
987	68	5.6	1021	2	CAB08737	Cab08737 mycobacte	1060	67.5	5.6	582	2	Q9JY58	Q9jy58 neisseria m
988	68	5.6	1056	2	Q7XFM6	Q7xfm6 oryza sativ	1061	67.5	5.6	585	2	Q9JT41	Q9jt41 neisseria m
989	68	5.6	1056	2	Q8S7A6	Q8s7a6 oryza sativ	1062	67.5	5.6	595	2	Q88TP0	Q88tp0 lactobacill
990	68	5.6	1075	2	Q7D5G6	Q7d5g6 mycobacteri	1063	67.5	5.6	596	1	POOB LYCES	Q88304 lycopersico
991	68	5.6	1085	2	Q6CBQ0	Q6cbq0 yarrowia li	1064	67.5	5.6	604	2	Q8VCK5	Q8vck5 mus musculu
992	68	5.6	1136	2	Q8K2V0	Q8k2v0 mus musculu	1065	67.5	5.6	604	2	Q6DPF6	Q6df6 xenopus lae
993	68	5.6	1157	1	XVNA_THESA	P36917 thermoanaer	1066	67.5	5.6	609	1	KHLX_HUMAN	Q9y2ms homo sapien
994	68	5.6	1173	2	Q63624	Q63624 rattus norv	1067	67.5	5.6	609	2	AAH63418	Aah63418 homo sapi
995	68	5.6	1304	2	Q8CMP6	Q8cmp6 pasteurella	1068	67.5	5.6	620	1	TYRO_NEUCR	Q6csy1 kluyveromyc
996	68	5.6	1523	1	DROL_THFEM	P74918 thermococcu	1069	67.5	5.6	642	2	Q6CSY1	Q6csy1 kluyveromyc
997	68	5.6	1524	2	Q9V854	Q9v854 drosophila	1070	67.5	5.6	663	2	Q7RVL7	Q7rvl7 neurospora
998	68	5.6	1866	1	SBFI_HUMAN	Q85248 homo sapien	1071	67.5	5.6	667	2	Q6R7E4	Q6r7e4 ostreid har
999	68	5.6	2266	1	POLI_TIGRVM	Q8b8x3 t rnal poly	1072	67.5	5.6	667	2	Q6R7E4	Q6r7e4 ostreid har
1000	68	5.6	2476	1	ZAN_PIG	Q82983 sus scrofa	1073	67.5	5.6	667	2	Q6R7E4	Q6r7e4 ostreid har
1001	68	5.6	5412	2	Q7R3N4	Q7r3n4 giardia lam	1074	67.5	5.6	685	2	AAH56974	Aah56974 mus muscu
1002	67.5	5.6	122	2	Q722A2	Q722a2 listeria mo	1075	67.5	5.6	685	2	Q6MGJ7	Q6mgj7 neurospora
1003	67.5	5.6	122	2	AAT03612	Aat03612 listeria	1076	67.5	5.6	685	2	CAE81941	Caes1941 neurospor
1004	67.5	5.6	154	2	Q7ZYU8	Q7zyu8 xenopus lae	1077	67.5	5.6	706	2	Q12296	Q12296 saccharomyc
1005	67.5	5.6	168	1	YXKA_BACSU	P55185 bacillus su	1078	67.5	5.6	754	2	P70847	P70847 bordetella
1006	67.5	5.6	188	2	Q6W2H8	Q6w2h8 rhizobium s	1079	67.5	5.6	763	2	Q9FKG5	Q9fkgs arabidopsi
1007	67.5	5.6	188	2	AAQ87039	Aa87039 rhizobium	1080	67.5	5.6	894	2	Q6PGK0	Q6pgk0 mus musculu
1008	67.5	5.6	204	2	Q3PBH4	Q3pbh4 xylella fas	1081	67.5	5.6	894	2	Q8CGA7	Q8cga7 mus musculu
1009	67.5	5.6	231	2	Q73EG6	Q73ec6 bacillus ce	1082	67.5	5.6	1004	2	Q7PQ53	Q7pq53 anopheles g
1010	67.5	5.6	231	2	AA539368	Aa539368 bacillus	1083	67.5	5.6	1010	1	HC58_MOUSE	Q8b1g0 mus musculu
1011	67.5	5.6	236	2	Q7CUB0	Q7cub0 agrobacteri	1084	67.5	5.6	1023	2	Q6PAR7	Q6par7 mus musculu
1012	67.5	5.6	236	2	Q8U895	Q8u895 agrobacteri	1085	67.5	5.6	1023	2	AAH60121	Aah60121 mus muscu
1013	67.5	5.6	236	2	Q8K2U3	Q8k2u3 mus musculu	1086	67.5	5.6	1034	2	Q8VHL7	Q8vhl7 mus musculu
1014	67.5	5.6	247	2	Q6FYX0	Q6fyx0 bartonella	1087	67.5	5.6	1034	2	Q8VHL7	Q8vhl7 mus musculu
1015	67.5	5.6	259	2	Q3D5K1	Q3d5k1 m mus muscu	1088	67.5	5.6	1050	2	Q7S1N5	Q7s1n5 neurospora
1016	67.5	5.6	265	2	Q8XIF5	Q8xyf5 hydra atten	1089	67.5	5.6	1058	2	Q873P1	Q873p1 emericella
1017	67.5	5.6	270	2	Q7QSS0	Q7qss0 giardia lam	1090	67.5	5.6	1118	2	Q8XV1	Q8xv1 uncultured
1018	67.5	5.6	271	2	Q7NDV3	Q7ndv3 mycobacter	1091	67.5	5.6	1242	2	Q8XRI5	Q8xri5 ralstonia s
1019	67.5	5.6	277	1	Y056_MYCCE	P47302 mycoplasma	1092	67.5	5.6	1247	2	Q7Q086	Q7q086 anopheles g
1020	67.5	5.6	289	2	Q739L9	Q739l9 bacillus ce	1093	67.5	5.6	1407	1	RPOC_XYLFA	Q9p8a7 xylella fas
1021	67.5	5.6	289	2	AA541042	Aa541042 bacillus	1094	67.5	5.6	1407	1	RPOC_XYLFT	Q9p8a7 xylella fas
1022	67.5	5.6	291	1	YF92_SYNY3	P72970 synechocyst	1095	67.5	5.6	1673	2	Q6MWC6	Q6mwc6 oryza sativ
1023	67.5	5.6	295	2	Q8S7P0	Q8s7p0 oryza sativ	1096	67.5	5.6	1726	2	Q7WKT6	Q7wkt6 borderella
1024	67.5	5.6	295	1	PUR7_STRAW	Q82fv6 streptomyce	1097	67.5	5.6	1729	2	Q7WTE7	Q7wte7 bordetella
1025	67.5	5.6	306	2	Q8P1S1	Q881s1 pseudomonas	1098	67.5	5.6	1729	2	Q8TKB8	Q8tkb8 methanosarc
1026	67.5	5.6	306	2	Q8PGN2	Q8pgn2 xanthomonas	1099	67.5	5.6	1939	2	Q9QBH1	Q9qbh1 viral hemor
1027	67.5	5.6	319	2	Q8XYO1	Q8xyo1 entamoeba h	1100	67.5	5.6	1984	2	Q9QBH5	Q9qbh5 viral hemor
1028	67.5	5.6	320	2	Q9ZBB0	Q9zbb0 sphingobium	1101	67.5	5.6	1984	2	Q9QJW0	Q9qjw0 viral hemor
1029	67.5	5.6	338	2	Q9ZII8	Q9zii8 streptomyce	1102	67.5	5.6	3988	2	Q8TP21	Q8tp21 methanosarc
1030	67.5	5.6	368	2	Q8C7G5	Q8c7g5 mus musculu	1103	67.5	5.6	41	2	Q9QV23	Q9qv23 rattus sp.
1031	67.5	5.6	368	2	Q99P64	Q99p64 mus musculu	1104	67.5	5.6	104	2	Q8DLR9	Q8dlr9 synechococc
1032	67.5	5.6	369	2	Q9SEX5	Q9sex5 canavalia l	1105	67.5	5.6	110	2	Q7XSE5	Q7xse5 erwinia rha
1033	67.5	5.6	377	2	Q8GHV5	Q8ghv5 pseudomonas	1106	67.5	5.6	145	2	Q83LV4	Q83lv4 shigella fl
1034	67.5	5.6	383	2	Q8MTN0	Q8mtn0 culicoides	1108	67.5	5.6	157	1	RSVR_COTJA	P98162 coturnix co
1035	67.5	5.6	385	2	Q8RLH5	Q8rlh5 fusobacteri	1109	67.5	5.6	158	1	YBHB_ECOLI	P12994 escherichia
1036	67.5	5.6	399	2	Q8RIR1	Q8rir1 paracoccus	1110	67.5	5.6	158	2	Q71HP4	Q71hp4 escherichia
1037	67.5	5.6	400	2	Q57407	Q57407 xenopus lae	1111	67.5	5.6	158	2	Q7AGD9	Q7agd9 escherichia
1038	67.5	5.6	436	2	Q8VDV6	Q8vdy6 mus musculu	1112	67.5	5.6	158	2	Q9APP3	Q9app3 uncultured
1039	67.5	5.6	437	2	Q8BK06	Q8bk06 mus musculu	1113	67.5	5.6	158	2	Q7UD98	Q7ud98 shigella fl
1040	67.5	5.6	444	2	Q8A599	Q8a599 bacteroides	1114	67.5	5.6	158	2	Q8FJQ8	Q8fjq8 escherichia
1041	67.5	5.6	453	2	Q6NVH6	Q6nyh6 brachydanio	1115	67.5	5.6	158	2	Q8Z895	Q8z895 salmonella
1042	67.5	5.6	453	2	AAH66589	Aah66589 brachydan	1116	67.5	5.6	158	2	Q8ZQ08	Q8zq08 salmonella
1043	67.5	5.6	454	2	Q9ZP23	Q9zp23 brassica ju	1117	67.5	5.6	158	2	Q8X828	Q8x828 escherichia
1044	67.5	5.6	472	1	SBPI_MOUSE	P17563 mus musculu	1118	67.5	5.6	158	2	AAQ07242	Aaq07242 escherich
1045	67.5	5.6	472	1	SYTM_MOUSE	Q8bvl4 mus musculu	1119	67.5	5.6	205	1	RS7_HALMA	P32552 haloarcula
1046	67.5	5.6	472	2	AAH60295	Aah60295 mus muscu	1120	67.5	5.6	218	2	Q7VUW6	Q7vuw6 bordetella
1047	67.5	5.6	475	2	Q6KAQ6	Q6kaq6 mus musculu	1121	67.5	5.6	218	2	Q7W329	Q7w329 bordetella
1048	67.5	5.6	475	2	BAD21401	Bad21401 mus muscu	1122	67.5	5.6	218	2	Q7WFD1	Q7wfd1 bordetella
1049	67.5	5.6	478	2	Q8EP49	Q8ep49 oceanobacill	1123	67.5	5.6	219	2	Q9LGS6	Q9lgs6 oryza sativ
1050	67.5	5.6	500	2	Q8JYD2	Q8jyd2 porcine lym	1124	67.5	5.6	242	2	Q29153	Q29153 vulpes vulp
1051	67.5	5.6	501	2	Q6BXN7	Q6bxm7 debaryomyce	1125	67.5	5.6	260	2	Q6MYB7	Q6myb7 aspergillus
1052	67.5	5.6	512	2	Q54400	Q54400 streptomyce	1126	67.5	5.6	260	2	CAF32086	Car32086 aspergill
1053	67.5	5.6	512	2	Q9RJ44	Q9rj44 streptomyce	1126	67.5	5.6	260	2	CAF32086	Car32086 aspergill

1127	67	5.6	274	2	Q7AF80	Q7af80 escherichia	1200	67	5.6	1661	2	Q7QQD8	Q7qqd8 giardia lam
1128	67	5.6	274	2	Q8PIN3	Q8fin3 escherichia	1201	67	5.6	1766	2	Q8AW45	Q8aw45 brachydanio
1129	67	5.6	274	2	Q8X866	Q8x866 escherichia	1202	67	5.6	2201	2	Q8IFQ5	Q8ifq5 plasmodium
1130	67	5.6	270	2	Q7UT29	Q7ut29 rhodopirell	1203	67	5.6	2552	2	Q9XCF2	Q9xcf2 mycobacteri
1131	67	5.6	290	2	Q752M4	Q752m4 ashbya goss	1204	67	5.6	4151	2	Q7D7J7	Q7d7j7 mycobacteri
1132	67	5.6	290	2	AAS53921	Aas53921 ashbya go	1205	67	5.6	4151	2	O53490	O53490 mycobacteri
1133	67	5.6	305	1	SVGA_VIBCH	Q8kvw7 vibrio chol	1206	67	5.6	4151	2	Q7VES2	Q7ves2 mycobacteri
1134	67	5.6	311	2	Q9K6F3	Q8k6w3 bacillus ha	1207	66.5	5.5	184	2	O42776	O42776 zygosacchar
1135	67	5.6	320	2	Q83YR4	Q83yr4 streptococc	1208	66.5	5.5	203	2	P95335	P95335 myxococcus
1136	67	5.6	346	2	Q9XIR1	Q9xir1 thermotoga	1209	66.5	5.5	240	2	P95E01	P95e01 xanthomonas
1137	67	5.6	348	2	Q9XPG1	Q9xpg1 gonostoma g	1210	66.5	5.5	243	2	Q72TF3	Q72tf3 leptospira
1138	67	5.6	361	2	O19635	Q19635 caenorhabdi	1211	66.5	5.5	243	2	AAS69675	Aas69675 leptospir
1139	67	5.6	367	2	Q9KTE1	Q8kte1 vibrio chol	1212	66.5	5.5	244	2	O8FIY1	O8fily1 leptospira
1140	67	5.6	369	2	O6K1Z1	Q8klz1 oryza sativ	1213	66.5	5.5	281	2	Q6FFA2	Q6ffa2 acinetobact
1141	67	5.6	369	2	BAD20140	Bad20140 oryza sat	1214	66.5	5.5	285	1	MIOX_HUMAN	Miox9b7 homo sapien
1142	67	5.6	372	1	CDK9_HUMAN	P50750 homo sapien	1215	66.5	5.5	285	2	Q967P6	Q967p6 gnathotrupe
1143	67	5.6	387	2	Q6TNI9	Q6tni9 nicotiana b	1216	66.5	5.5	285	2	CAG30364	Cag30364 homo sapi
1144	67	5.6	387	2	AAQ91380	Aaq91380 nicotiana	1217	66.5	5.5	289	2	O813N9	O813n9 bacillus ce
1145	67	5.6	389	2	O9LT21	O9lt21 arabidopsis	1218	66.5	5.5	297	2	Q45090	Q45090 burkholderi
1146	67	5.6	396	2	Q9SD25	Q9sd25 oryza sativ	1219	66.5	5.5	309	2	Q7AX06	Q7ax06 neisseria m
1147	67	5.6	400	2	O89NL3	Q89nl3 bradyrhizob	1220	66.5	5.5	309	2	Q9JRI9	Q9jri9 neisseria m
1148	67	5.6	403	2	Q9U250	Q9u250 caenorhabdi	1221	66.5	5.5	320	2	Q9AIS1	Q9ais1 sphingomona
1149	67	5.6	407	2	O8BS18	Q8bs18 mus musculu	1222	66.5	5.5	326	2	Q7XT82	Q7xt82 oryza sativ
1150	67	5.6	407	2	O8CGV1	Q8cgv1 mus musculu	1223	66.5	5.5	328	1	Y630_STRP3	Y630_strp3 streptococc
1151	67	5.6	412	1	LVA3_HUMAN	O8ncc3 homo sapien	1224	66.5	5.5	328	1	Y915_STRPY	Y915_strpy streptococc
1152	67	5.6	412	2	AAH2605	Aah2605 homo sapi	1225	66.5	5.5	328	1	YF04_STRA3	Yf04_stra3 streptococc
1153	67	5.6	431	1	TRPB_DEIRA	Q9rvti deinococcus	1226	66.5	5.5	330	2	Q7QEW5	Q7qew5 anopheles g
1154	67	5.6	458	2	Q9RHA5	Q9rha5 pseudomonas	1227	66.5	5.5	346	2	Q7LXX7	Q7lxx7 schizosacch
1155	67	5.6	459	2	Q747H0	Q747h0 geobacter s	1228	66.5	5.5	354	2	Q6C7H2	Q6c7h2 yarrowia li
1156	67	5.6	459	2	AA36686	Aar36686 geobacter	1229	66.5	5.5	355	2	O8RD34	O8rd34 thermoanaer
1157	67	5.6	465	1	APR1_ARATH	P92979 a 5'-adenyl	1230	66.5	5.5	368	2	Q9IX90	Q9ix90 mus musculu
1158	67	5.6	465	2	O8L6A0	Q8la60 arabidopsis	1231	66.5	5.5	387	2	Q9P8Z7	Q9p8z7 spirotyces
1159	67	5.6	465	2	AAO11528	Q60000 rattus norv	1232	66.5	5.5	389	1	YP46_RTBPV	Yp46_rtbvp rice tungro
1160	67	5.6	474	1	L1PL_RAT	P55031 felis silve	1233	66.5	5.5	391	2	Q9V6S7	Q9v6s7 homo sapien
1161	67	5.6	478	1	L1PL_FELCA	P55031 felis silve	1234	66.5	5.5	402	1	HCYB_HELPO	Hcyb_helpo arabidopsis
1162	67	5.6	484	2	O8PAP4	O8pap4 xanthomonas	1235	66.5	5.5	410	1	Q89G99	Q89g99 bradyrhizob
1163	67	5.6	488	2	Q7QJ30	Q7qj30 anopheles g	1236	66.5	5.5	412	2	Q89G99	Q89g99 bradyrhizob
1164	67	5.6	493	2	Q7C2N9	Q7c2n9 shigella fl	1237	66.5	5.5	418	2	Q7UP54	Q7up54 rhodopirell
1165	67	5.6	493	2	Q83884	Q83884 shigella fl	1238	66.5	5.5	429	2	Q9SAD0	Q9sad0 arabidopsis
1166	67	5.6	497	2	O6LKY2	Q6lky2 photobacter	1239	66.5	5.5	451	2	Q8UUU0	Q8uuu0 gallus gall
1167	67	5.6	497	2	CAG22029	Cag22029 photobact	1240	66.5	5.5	459	1	RN25_HUMAN	Rn25_humo sapien
1168	67	5.6	505	1	MAL3_DROME	P07192 drosophila	1241	66.5	5.5	487	2	Q7SHA3	Q7sha3 neurospora
1169	67	5.6	545	2	O6UIQ2	O6ulq2 novumbra hu	1242	66.5	5.5	495	1	GATB_HALN1	Gatb_haln1 halobacteri
1170	67	5.6	545	2	AA275500	Aar27500 novumbra	1243	66.5	5.5	528	2	Q7QTE9	Q7qte9 giardia lam
1171	67	5.6	556	2	Q53641	Q53641 sulfolobus	1244	66.5	5.5	532	1	INV1_YEAST	Iv10594 saccharomyc
1172	67	5.6	567	1	TR3_MOUSE	Q60803 mus musculu	1245	66.5	5.5	532	1	Q6H960	Q6h960 saccharomyc
1173	67	5.6	568	1	TR3_HUMAN	Q13114 homo sapien	1246	66.5	5.5	546	2	O6UIQ6	O6ulq6 esox lucius
1174	67	5.6	571	1	V096_FOWPV	Q9j5c4 fowlpox vir	1247	66.5	5.5	546	2	AA27496	Aar27496 esox luci
1175	67	5.6	571	2	Q70H58	Q70h58 fowlpox vir	1248	66.5	5.5	583	2	Q8FTC8	Q8ftc8 methanosarc
1176	67	5.6	571	2	CAE52638	Caes2638 fowlpox v	1249	66.5	5.5	608	2	Q829A8	Q829a8 streptomyce
1177	67	5.6	619	2	Q6BIU3	Q6biu3 debaryomyce	1250	66.5	5.5	611	2	Q9QWN7	Q9qwn7 rattus norv
1178	67	5.6	632	2	Q7S616	Q7s616 neurospora	1251	66.5	5.5	637	2	O33838	O33838 thermotoga
1179	67	5.6	674	1	CAN9_RAT	Q35920 rattus norv	1252	66.5	5.5	639	2	Q9S5X2	Q9s5x2 thermotoga
1180	67	5.6	678	1	MPH1_SCHPO	Q94235 schizosacch	1253	66.5	5.5	640	2	O6F860	O6f860 acinetobact
1181	67	5.6	691	2	Q7ZU98	Q7zu98 brachydanio	1254	66.5	5.5	649	2	Q8PBW1	Q8pbw1 xanthomonas
1182	67	5.6	728	2	O8BD11	Q8bdi1 m mus muscu	1255	66.5	5.5	720	2	Q9DUB7	Q9dub7 tt virus. o
1183	67	5.6	732	2	Q9NV66	Q9nv66 homo sapien	1256	66.5	5.5	725	2	Q9JXU3	Q9jxu3 neisseria m
1184	67	5.6	737	1	DP3_HUMAN	Q9ny33 homo sapien	1257	66.5	5.5	790	2	Q20599	Q20599 caenorhabdi
1185	67	5.6	751	2	Q7ZU06	Q7zu06 brachydanio	1258	66.5	5.5	793	1	SYFB_CLOPE	Syfb_clostridium
1186	67	5.6	753	2	Q6ZSB4	Q6zsb4 homo sapien	1259	66.5	5.5	842	2	O9SQF5	O9sqf5 caenorhabdi
1187	67	5.6	753	2	Q90WS1	Q90wsl fugu rubrip	1260	66.5	5.5	848	2	Q8H962	Q8h962 zinnia eleg
1188	67	5.6	733	2	BAC87040	Bac87040 homo sapi	1261	66.5	5.5	849	2	Q8VX29	Q8vx29 zinnia eleg
1189	67	5.6	759	2	Q8K2G0	Q8k2g0 mus musculu	1262	66.5	5.5	956	1	CYLD_HUMAN	Cyld_homo sapien
1190	67	5.6	793	2	Q92819	Q92819 listeria in	1263	66.5	5.5	963	2	Q9LS91	Q9ls91 arabidopsis
1191	67	5.6	804	2	Q8N885	Q8n885 homo sapien	1264	66.5	5.5	964	2	Q7SEG3	Q7seg3 ashbya goss
1192	67	5.6	812	1	PDAL_MAIZE	Q43270 zea mays (m	1265	66.5	5.5	964	2	AAS50481	Aas50481 ashbya go
1193	67	5.6	814	2	Q87V08	Q87v08 pseudomonas	1266	66.5	5.5	973	2	O86728	O86728 streptomyce
1194	67	5.6	829	2	Q8CDN0	Q8cdn0 mus musculu	1267	66.5	5.5	1030	2	O875U4	O875u4 saccharomyc
1195	67	5.6	841	2	Q44207	Q44207 agrobacteri	1268	66.5	5.5	1031	2	Q80YN7	Q80yn7 mus musculu
1196	67	5.6	857	2	Q82CF5	Q82cf5 streptomyce	1269	66.5	5.5	1047	2	Q6C109	Q6c109 yarrowia li
1197	67	5.6	967	2	Q6CB57	Q6cb57 yarrowia li	1270	66.5	5.5	1064	1	CARB_LACLC	C32771 lactococcus
1198	67	5.6	1614	2	Q75GM6	Q75gm6 oryza sativ	1271	66.5	5.5	1066	2	Q8S464	Q8s464 zea mays (m
1199	67	5.6	1614	2	AAT01370	Aat01370 oryza sat	1272	66.5	5.5	1077	1	CARB_VIBPA	Q878f3 vibrio para

1273	1273	66.5	5.5	1129	2	Q80UX0	Q80ux0 mus musculus	1346	66	5.5	493	2	Q7AGL2	Q7agL2 escherichia
1274	1274	66.5	5.5	1179	2	Q9N8M4	Q9n8m4 trypanosoma	1347	66	5.5	493	2	Q8X9D3	Q8x9d3 escherichia
1275	1275	66.5	5.5	1305	2	Q7PSN5	Q7pns5 anopheles g	1348	66	5.5	501	2	Q8IGP1	Q8igp1 drosophila
1276	1276	66.5	5.5	1336	2	Q9ESH4	Q9esh4 mus musculus	1349	66	5.5	501	2	Q6NV47	Q6nv47 mus musculus
1277	1277	66.5	5.5	1341	2	Q9ULE5	Q9ule5 leishmania	1350	66	5.5	501	2	Q8CE2	Q8ce2 mus musculus
1278	1278	66.5	5.5	1342	1	CND1_MOUSE	Q8k2z4 mus musculus	1351	66	5.5	501	2	Q8CA30	Q8ca30 mus musculus
1279	1279	66.5	5.5	1392	1	Q6ZQI1	Q6zqi1 mus musculus	1352	66	5.5	501	2	Q8CAL3	Q8cal3 mus musculus
1280	1280	66.5	5.5	1397	2	BAC97878	Bac97878 mus muscu	1353	66	5.5	501	2	Q8CBW4	Q8cbw4 mus musculus
1281	1281	66.5	5.5	1426	2	Q6ZGV8	Q6zgv8 oryza sativ	1354	66	5.5	501	2	AAO41256	AAo41256 drosophila
1282	1282	66.5	5.5	1426	2	BAD09184	Bad09184 oryza sat	1355	66	5.5	501	2	AAH68319	AAh68319 mus muscu
1283	1283	66.5	5.5	1426	2	BAD12895	Bad12895 oryza sat	1356	66	5.5	502	2	Q8CBX8	Q8cbx8 mus musculus
1284	1284	66.5	5.5	1455	2	Q6ZPU4	Q6zpu4 mus musculus	1357	66	5.5	507	2	Q8P5H0	Q8p5h0 xanthomonas
1285	1285	66.5	5.5	1455	2	BAC98135	Bac98135 mus muscu	1358	66	5.5	520	2	Q8UFI3	Q8ufi3 agrobacteri
1286	1286	66.5	5.5	1561	2	Q924D2	Q924d2 mus musculus	1359	66	5.5	528	2	Q6K7L3	Q6k7l3 oryza sativ
1287	1287	66.5	5.5	1578	2	Q616G8	Q616g8 mus musculus	1360	66	5.5	528	2	BAD19496	BAd19496 oryza sat
1288	1288	66.5	5.5	1717	2	Q7PFF8	Q7pff8 anopheles g	1361	66	5.5	544	2	Q9NUL8	Q9nul8 homo sapien
1289	1289	66.5	5.5	1940	2	Q6PDN3	Q6pdn3 mus musculus	1362	66	5.5	547	2	Q7CZB0	Q7czb0 agrobacteri
1290	1290	66.5	5.5	1940	2	AAH58610	Aah58610 mus muscu	1363	66	5.5	560	2	Q9H8A6	Q9h8a6 homo sapien
1291	1291	66.5	5.5	1950	2	Q80YN8	Q80yn8 mus musculus	1364	66	5.5	561	2	Q9H9C4	Q9h9c4 homo sapien
1292	1292	66.5	5.5	2193	2	Q9WPU0	Q9wpj0 human enter	1365	66	5.5	574	2	Q9V4T8	Q9v4t8 drosophila
1293	1293	66.5	5.5	2193	2	Q9WQU0	Q9wgj0 human enter	1366	66	5.5	592	2	Q6MKJ7	Q6mkj7 bdellovibri
1294	1294	66.5	5.5	2193	2	Q9QF52	Q9qf52 human enter	1367	66	5.5	592	2	CAE80210	CAe80210 bdellovib
1295	1295	66.5	5.5	2193	2	Q9QRL8	Q9qrl8 human enter	1368	66	5.5	593	2	Q78FQ7	Q78fq7 neurospora
1296	1296	66.5	5.5	2193	2	Q9DY01	Q9dy01 human enter	1369	66	5.5	607	2	Q74ZC8	Q74zc8 ashbya goss
1297	1297	66.5	5.5	2193	2	Q9DY02	Q9dy02 human enter	1370	66	5.5	607	2	Q74ZC8	Q74zc8 ashbya goss
1298	1298	66.5	5.5	2858	2	Q81AK2	Q8iak2 plasmodium	1371	66	5.5	635	1	SYT_RICPR	AA54761 ashbya go
1299	1299	66.5	5.5	3358	1	PGCV_MOUSE	Q62059 mus musculus	1372	66	5.5	638	2	Q9Z389	Q9z389 streptomyce
1300	1300	66	5.5	160	2	Q8C2Z4	Q8c2z4 mus musculus	1373	66	5.5	642	2	Q8EER9	Q8eer9 shewanella
1301	1301	66	5.5	169	2	Q8CVN3	Q8cvn3 escherichia	1374	66	5.5	647	1	CN16_SALTY	P26265 salmonella
1302	1302	66	5.5	186	1	THM2_ARATH	Q9seu8 arabidopsis	1375	66	5.5	654	2	Q87JM4	Q87jm4 vibrio para
1303	1303	66	5.5	186	2	AAK76675	Aak76675 arabidops	1376	66	5.5	654	2	Q989X2	Q989x2 rhizobium l
1304	1304	66	5.5	186	2	AAH85093	AAh85093 arabidops	1377	66	5.5	665	1	GAK2_HUMAN	Q989x2 rhizobium l
1305	1305	66	5.5	197	2	Q83ZK7	Q83zr7 corynebacte	1378	66	5.5	685	1	GAK5_HUMAN	Q6myu6 aspergillus
1306	1306	66	5.5	210	2	Q70JC5	Q70jc5 bacillus li	1379	66	5.5	680	2	Q6MYU6	CAE47913 aspergill
1307	1307	66	5.5	210	2	CAE17299	CAe17299 bacillus	1380	66	5.5	692	2	Q8YZQ2	Q8yzq2 anabaena sp
1308	1308	66	5.5	219	2	Q81957	Q819e7 bacillus ce	1381	66	5.5	702	2	Q8NDB8	Q8ndb8 homo sapien
1309	1309	66	5.5	226	2	Q9KYV0	Q9kyv0 streptomyce	1382	66	5.5	706	1	MR11_RAT	Q9jim0 rattus norv
1310	1310	66	5.5	238	2	Q67863	Q67863 aquifex ae	1383	66	5.5	712	2	Q7X8E0	Q7x8e0 oryza sativ
1311	1311	66	5.5	247	2	Q7NEA7	Q7neat7 agrobacter	1384	66	5.5	712	2	CA503464	CAe03464 oryza sat
1312	1312	66	5.5	256	2	Q9XGR7	Q9xgr7 streptomyce	1385	66	5.5	716	2	Q71EE0	Q71ee0 agrobacteri
1313	1313	66	5.5	262	2	Q7Q7Q1	Q7q7q1 anopheles g	1386	66	5.5	716	2	AAQ08598	AAq08598 agrobacte
1314	1314	66	5.5	263	2	Q96RN6	Q96rn6 homo sapien	1387	66	5.5	717	2	Q9QP18	Q9qp18 gallid herp
1315	1315	66	5.5	276	2	Q7MAZ9	Q7maz9 bordetella	1388	66	5.5	738	1	PLAP_HUMAN	Q9y263 homo sapien
1316	1316	66	5.5	296	2	Q8NBR1	Q8nbr1 homo sapien	1389	66	5.5	738	2	Q81TK7	Q81tk7 streptomyce
1317	1317	66	5.5	304	2	Q9RFU7	Q9rfj7 sphingopyxi	1390	66	5.5	751	2	Q8AYN4	Q8ayn4 brachydanio
1318	1318	66	5.5	309	2	Q6CUK3	Q6cuk3 kluveromyce	1391	66	5.5	770	2	Q49846	Q49846 egeria dens
1319	1319	66	5.5	311	2	Q8YF20	Q8yp20 anabaena sp	1392	66	5.5	775	1	DPOL_THES9	Q56366 thermococcu
1320	1320	66	5.5	350	2	Q8YRB6	Q8yrb6 anabaena sp	1393	66	5.5	776	2	Q9SH68	Q9sh68 arabidopsis
1321	1321	66	5.5	375	2	Q8FJ35	Q8fj35 escherichia	1394	66	5.5	779	2	Q831Q3	Q83lq3 enterococcu
1322	1322	66	5.5	380	2	Q6NZT4	Q6nzt4 brachydanio	1395	66	5.5	795	2	Q9UF53	Q9uf53 homo sapien
1323	1323	66	5.5	380	2	AAH65977	Aah65977 brachydan	1396	66	5.5	795	2	Q9NVE9	Q9nve9 homo sapien
1324	1324	66	5.5	381	2	Q84GI2	Q84gi2 enterobacte	1397	66	5.5	895	2	BAC34837	BAC34837 m 12 days
1325	1325	66	5.5	381	2	Q84G13	Q84g13 enterobacte	1398	66	5.5	1005	1	EVC_MOUSE	P57680 mus musculus
1326	1326	66	5.5	395	2	Q70W04	Q70w04 thermoprote	1399	66	5.5	1042	2	Q55528	Q55528 synchocyst
1327	1327	66	5.5	395	2	CAD56501	Cad56501 thermopro	1400	66	5.5	1065	2	Q7TVU1	Q7tvu1 mycobacteri
1328	1328	66	5.5	401	1	CARA_AGR75	Q8udt7 agrobacteri	1401	66	5.5	1077	2	Q8TE71	Q8ts71 homo sapien
1329	1329	66	5.5	420	2	Q6C831	Q6c831 yarrowia li	1402	66	5.5	1078	2	Q9A3J0	Q9a3j0 caulobacter
1330	1330	66	5.5	423	2	Q8Z0X2	Q8z0x2 salmonella	1403	66	5.5	1095	2	Q913U4	Q913u4 pseudomonas
1331	1331	66	5.5	423	2	Q8ZJ25	Q8zj25 salmonella	1404	66	5.5	1098	2	Q75EP5	Q75ep5 ashbya goss
1332	1332	66	5.5	443	2	Q9HAL4	Q9hal4 homo sapien	1405	66	5.5	1098	2	Q75EP5	Q75ep5 ashbya goss
1333	1333	66	5.5	455	2	Q8A354	Q8a354 bacteroides	1406	66	5.5	1098	2	AA550399	AA550399 ashbya go
1334	1334	66	5.5	457	2	Q6PHD9	Q6phd9 brachydanio	1407	66	5.5	1126	2	Q61MN5	Q61mn5 homo sapien
1335	1335	66	5.5	457	2	AAH56590	Aah56590 brachydan	1408	66	5.5	1127	2	Q61MN6	Q61mn6 homo sapien
1336	1336	66	5.5	462	2	Q86BH9	Q86bh9 drosophila	1409	66	5.5	1189	2	Q8C867	Q8c867 yarrowia li
1337	1337	66	5.5	462	2	AAO41260	AAo41260 drosophil	1410	66	5.5	1194	2	Q9R6F0	Q9rf60 agrobacteri
1338	1338	66	5.5	466	2	Q9USN2	Q9usn2 schizosacch	1411	66	5.5	1391	2	Q7ZXT3	Q7zxt3 xenopus lae
1339	1339	66	5.5	475	2	Q96FC4	Q96fc4 homo sapien	1412	66	5.5	1495	2	Q94CX4	Q94cx4 oryza sativ
1340	1340	66	5.5	475	2	Q94VY3	Q94vy3 arabidopsis	1413	66	5.5	1520	2	O15829	O15829 leishmania
1341	1341	66	5.5	476	2	Q7PGF1	Q7pgf1 anopheles g	1414	66	5.5	1524	2	Q91830	Q91830 trypanosoma
1342	1342	66	5.5	477	2	Q96JF4	Q96jf4 homo sapien	1415	66	5.5	1613	2	Q9NLR0	Q9nlr0 leishmania
1343	1343	66	5.5	479	2	Q8H3X8	Q8h3x8 oryza sativ	1416	66	5.5	1713	2	Q9VRG4	Q9vr94 drosophila
1344	1344	66	5.5	493	1	YBGH_ECOLI	P75742 escherichia	1417	66	5.5	2089	2	Q39478	Q39478 cyclorella
1345	1345	66	5.5	493	2	Q9N889	Q9n889 plasmodium	1418	66	5.5	2311	2	Q6DNF2	Q6dnf2 lyngbya maj

1419	66	5.5	2326	1	PGG2_RAT	Q00657 rattus norv
1420	66	5.5	2462	2	Q7QT93	Q8t93 giardia lam
1421	66	5.5	2478	2	Q8YTN5	Q8Ytn5 anabaena sp
1422	66	5.5	2834	2	Q20456	Q20456 caenorhabdi
1423	66	5.5	3068	1	POLG_PEMVC	Q01500 p genome po
1424	66	5.5	3068	2	Q8JRG5	Q8jrs5 pepper mott
1425	65.5	5.4	122	2	Q8ZJF9	Q8zjf9 yersinia pe
1426	65.5	5.4	122	2	AAN09537	Aan09537 drosophil
1427	65.5	5.4	124	1	YE22_RHIME	Q92qb2 thizobium m
1428	65.5	5.4	142	2	Q8CK96	Q8ck96 yersinia p
1429	65.5	5.4	142	2	AAS60428	Aas60428 yersinia
1430	65.5	5.4	159	1	HS12_DAUCA	P27397 daucus caro
1431	65.5	5.4	161	2	Q9HJ86	Q9hj86 thermoplas
1432	65.5	5.4	169	2	Q8DST0	Q8dst0 streptococ
1433	65.5	5.4	179	2	Q938C7	Q938c7 mycobacteri
1434	65.5	5.4	195	1	COAG_LIMPO	P03998 limulus pol
1435	65.5	5.4	198	1	LOLA_VIBVY	Q7mlv4 vibrio vuln
1436	65.5	5.4	199	2	Q88L82	Q88lb2 pseudomonas
1437	65.5	5.4	199	2	Q9D1X5	Q9dlx5 m mus muscu
1438	65.5	5.4	204	2	Q8LR35	Q8lrs5 oryza sativ
1439	65.5	5.4	224	2	Q9ZHL5	Q9zh15 desulfotoma
1440	65.5	5.4	224	2	Q7T5F2	Q7t5f2 cercopithe
1441	65.5	5.4	236	2	Q7Z3V4	Q7z3v4 homo sapien
1442	65.5	5.4	243	2	Q806C8	Q806c8 cercopithe
1443	65.5	5.4	255	2	Q9B074	Q9b074 mycobacteri
1444	65.5	5.4	262	2	Q9RC64	Q9rc64 bacillus ha
1445	65.5	5.4	266	2	Q09514	Q09514 caenorhabdi
1446	65.5	5.4	279	1	PANC_CORGL	Q9x713 corynebacte
1447	65.5	5.4	293	2	Q8FN14	Q8fn14 corynebacte
1448	65.5	5.4	294	2	Q83GB6	Q83gb6 tropheryma
1449	65.5	5.4	294	2	Q83HW2	Q83hw2 tropheryma
1450	65.5	5.4	309	2	Q7ZU03	Q7zu03 brachydanio
1451	65.5	5.4	315	2	Q8F249	Q8f249 leptospira
1452	65.5	5.4	353	2	Q9TQD5	Q9tgds cuturnix co
1453	65.5	5.4	361	2	Q8WPA2	Q8wpa2 bombyx mori
1454	65.5	5.4	364	2	Q6MB12	Q6mb12 parachlamyd
1455	65.5	5.4	364	2	CAF24237	CAF24237 parachlam
1456	65.5	5.4	368	2	Q9A3K5	Q9a3r5 caulobacter
1457	65.5	5.4	372	1	SHAK_DROME	P33085 drosophila
1458	65.5	5.4	375	1	YCDFO_ECOLI	P75902 escherichia
1459	65.5	5.4	375	2	Q7AFW5	Q7afw5 escherichia
1460	65.5	5.4	375	2	Q8XAS6	Q8xas6 escherichia
1461	65.5	5.4	376	1	CEA2_RAT	Q9jki5 rattus norv
1462	65.5	5.4	404	2	Q7FAK6	Q7far6 oryza sativ
1463	65.5	5.4	404	2	Q94FB5	Q94fb5 oryza sativ
1464	65.5	5.4	409	2	Q28222	Q28222 archaeoglob
1465	65.5	5.4	420	2	Q6W958	Q6w958 octopus rub
1466	65.5	5.4	420	2	AQW72761	Aaq72761 octopus r
1467	65.5	5.4	423	2	Q9KFY7	Q9kfy7 bacillus ha
1468	65.5	5.4	429	2	Q8LC35	Q8lc35 arabidopsis
1469	65.5	5.4	431	2	Q7SY92	Q7sy92 xenopus lae
1470	65.5	5.4	433	1	1HK1_MOUSE	Q6pd10 mus musculu
1471	65.5	5.4	433	2	AAH59006	AAH59006 mus muscu
1472	65.5	5.4	435	2	Q9LO80	Q9lq80 arabidopsis
1473	65.5	5.4	437	2	Q8T015	Q8t015 drosophila
1474	65.5	5.4	445	1	BPI_RABIT	Q8t739 oryctolegus
1475	65.5	5.4	448	2	Q9KDR4	Q9kdr4 bacillus ha
1476	65.5	5.4	450	2	Q6I7B6	Q6i7b6 pyrococcus
1477	65.5	5.4	456	1	E2B_AQUAE	Q67879 aquifex aeo
1478	65.5	5.4	458	2	Q84EP4	Q84ep4 wautersia o
1479	65.5	5.4	459	1	RSP6_CHLRE	Q01657 chlamydomon
1480	65.5	5.4	469	1	YJL1_CABEL	P34366 caenorhabdi
1481	65.5	5.4	471	2	Q8BM72	Q8bm72 mus musculu
1482	65.5	5.4	472	2	Q8VIF7	Q8vif7 rattus norv
1483	65.5	5.4	480	2	Q75L15	Q75ll15 oryza sativ
1484	65.5	5.4	480	2	AAR87254	Aar87254 oryza sat
1485	65.5	5.4	504	1	OPGG_RALSO	Q8xvc3 ralsstonia s
1486	65.5	5.4	509	2	Q7YMW1	Q7ymv1 clematis vi
1487	65.5	5.4	509	2	Q7YMW9	Q7ymv9 clostridius
1488	65.5	5.4	520	2	Q8GH59	Q8gh59 clostridius
1489	65.5	5.4	540	2	Q75BA2	Q75ba2 ashbya goss
1490	65.5	5.4	540	2	AAS51584	Aas51584 ashbya go
1491	65.5	5.4	542	2	Q59145	Q59145 aeromonas s

ALIGNMENTS

RESULT 1

ID	BPPL HUMAN	STANDARD;	PRT;	223 AA.
AC	Q96S56; Q8W74;			
DT	05-JUL-2004 (Rel. 44, Created)			
DT	05-JUL-2004 (Rel. 44, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	PBP family protein precursor (UNQ1933/PRO4408)			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RL	Zhang W., Li N., Wan T., Cao X.;			
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.P., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Eaton D., Fostor J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,			
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,			
RA	Godowski P., Gray A.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment."			
RL	Genome Res. 13:2265-2270(2003).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RX	MEDLINE=22887297; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.-I., Wang J., Haieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Faney J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywicki M.I., Skalek U., Smailus D.E.,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
CC	-I- SUBCELLULAR LOCATION: Secreted (Potential).			
CC	-I- SIMILARITY: Belongs to the phosphatidylethanolamine-binding			
CC	protein family.			


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EMBL: AY037148; AAK67629.1; -
EMBL: AY359109; AAO89467.1; -
EMBL: BC020779; AAH20779.1; -
HSSP: P13696; 1A44.
InterPro: IPR001858; PBP.
InterPro: IPR008914; PEBP.
Pfam: PF01161; PBP; 1.
ProDom: PD004330; PBP; 1.
PROSITE: PS01220; PBP; 1.
Signal.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 223 PBP family protein.
FT CONFLICT 125 125 E -> K (in Ref. 2).
FT CONFLICT 211 211 G -> E (in Ref. 1).
FT CONFLICT 220 223 TRRR -> NQAEIAAC (in Ref. 1).
FT CONFLICT 222 222 R -> Q (in Ref. 2).
SQ SEQUENCE 223 AA; 25431 MW; 9139E4AB8241A4F8 CRC64;

Query Match 99.3%; Score 1196; DB 1; Length 223;
Best Local Similarity 99.1%; Pred. No. 4.4e-107;
Matches 221; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWMLRLVTAALLGLMMVVTGDEDENSPCAEHALLDEDTLFCQGLEVFYFPELGNICKV 60
DB 1 MGWMLRLVTAALLGLMMVVTGDEDENSPCAEHALLDEDTLFCQGLEVFYFPELGNICKV 60

QY 61 VPDCCNYRQKITSWMEPIKPGAVDGYTYLLVWVDPDPSRAPRPRFRWHMLVTDIKG 120
DB 61 VPDCCNYRQKITSWMEPIKPGAVDGYTYLLVWVDPDPSRAPRPRFRWHMLVTDIKG 120

QY 121 ADLAKGKIQOGLSAYQAPSPAHSGFHRVYFFVYLOEGKVISLLPKENTRGSWKMDRF 180
DB 121 ADLAKGKIQOGLSAYQAPSPAHSGFHRVYFFVYLOEGKVISLLPKENTRGSWKMDRF 180

QY 181 LNRHFLGPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTROR 223
DB 181 LNRHFLGPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRRR 223

RESULT 2
PBPL_MOUSE STANDARD; PRT; 242 AA.
ID PBPL_MOUSE
AC Q9D9G2;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE PBP family protein precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriell L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Bruscia V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

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RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perteau G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reid J.J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: Belongs to the phosphatidylinositolamine-binding
CC protein family.
-----
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EMBL: AK005964; BAB24810.1; -
HSSP: P30086; 1BD9.
MGD: MGI:1920773; 1700081D17Rik.
InterPro: IPR001858; PBP.
InterPro: IPR008914; PEBP.
Pfam: PF01161; PBP; 1.
ProDom: PD004330; PBP; 1.
PROSITE: PS01220; PBP; 1.
Signal.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 242 PBP family protein.
FT SEQUENCE 242 AA; 26908 MW; 21796A1755FAF01B CRC64;

Query Match 46.6%; Score 561.5; DB 1; Length 242;
Best Local Similarity 46.3%; Pred. No. 8.9e-46;
Matches 113; Conservative 37; Mismatches 67; Indels 27; Gaps 4;

QY 4 TMRLVTAALLGLM-----MVVTGDE-DENSP-----CAHEALLDED 39
DB 2 TMKLVAALCLLLAAGLWVGLSLTAESIEGKPGEGKPGSGRGGLPLPKED 61

QY 40 TLFCQGLEVFYFPELGNICKVVDCCNYRQKITSWMEPIKPGAVDGYTYLLVWVDPDA 99
DB 62 VSLCENLEVFYFMEGNIISKIVPKCNLYRQKIPAMQAPIVKFTALDGLYLLVWVDPDA 121

QY 100 PSRAPRPRFRWHMLVTDIKADLKKGIQOGLSAYQAPSPAHSGFHRVYFFVYLOEG 159
DB 122 PSRSNPNVWKYHWHLVSNITGADMKSGSIRGNVLSDYSPTTPTGTVHRTQFFVYLOEG 181

QY 160 KVISLLPKENTRGSWKMDRFNLRHFLGPEASTQFMTQNYQDSPTLQAPRGRASEPKHK 219
DB 182 RDISLSVEEKANLGWNLDKFLQYGLRDPDSTQFMTQFDEE---LSSEGRINDDQEQ 238.

QY 220 TFQR 223
DB 239 FNQK 242

RESULT 3
Q86PT6 PRELIMINARY; PRT; 211 AA.
Q86PT6
ID Q86PT6

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AC Q86PT6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative antennal carrier protein A5.
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14986919;
RA Justice R., Dimitratos S., Walter M.F., Woods D.F., Biessmann H.;
RT "Sexual dimorphic expression of putative antennal carrier protein
RT genes in the malaria vector Anopheles gambiae.";
RL Insect Mol. Biol. 12:581-594 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Justice R., Dimitratos S., Walter M.F., Woods D.F., Biessmann H.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY187040; AAC039754.1; -.
DR HSSP; Q8VIN1; IKN3.
DR InterPro; IPR008914; PEBP.
DR Pfam; PF01161; PBP; 1.
DR ProDom; PD004330; PBP; 1.
SQ SEQUENCE 211 AA; 23141 MW; 79784263A4DAC45E CRC64;

Query Match 21.6%; Score 260.5; DB 2; Length 211;
Best Local Similarity 33.9%; Pred. No. 8.6e-17;
Matches 58; Conservative 26; Mismatches 68; Indels 19; Gaps 4;

QY 44 QGLEVFYFELG---NIGCKVVPDCNNYRQKITSMWEPVFKPGAVDGAATYILVMVDPDAP 100
DB 48 QTIKIYTPQSDVEVSLGNQLTPTQVKARPKLWHEVEP-----SALTLLMADPDAP 98
QY 101 SRAEPQRFWRHVLVTDIKADLKGKIQGQELSAVOAPSPAHSGFHRFYOFFVYLQEGK 160
DB 99 SRSNPNRWSKHWLVGNIPGADV-----LADYVSGSPGPGTGLHRYVFLVYKQPSR 154
QY 161 VI---SLLPKENKTRGSKMDRLNRFHLGPEASTQFMNTQYQDSPTLQA 208
DB 155 IVFNETVLSRNPNGKWNPAEFVKEVGLGVPVAGNFYQAYQDYDYPVELYA 205

RESULT 4
Q7QHW0 PRELIMINARY; PRT; 224 AA.
AC Q7QHW0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AgCP7981 (Fragment).
GN Name=agCG44359; ORFNames=ENSANGG00000014792;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -/- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAA01008813; EAA04988.1; -.
DR InterPro; IPR008914; PEBP.
DR Pfam; PF01161; PBP; 1.
DR ProDom; PD004330; PBP; 1.
FT NON TER 1
SQ SEQUENCE 224 AA; 24783 MW; 0C1BC0BA67224D85 CRC64;

Query Match 21.5%; Score 258.5; DB 2; Length 224;
Best Local Similarity 33.9%; Pred. No. 8.6e-17;
Matches 58; Conservative 26; Mismatches 68; Indels 19; Gaps 4;
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Best Local Similarity 33.9%; Pred. No. 1.4e-16;
Matches 58; Conservative 26; Mismatches 68; Indels 19; Gaps 4;

QY 44 QGLEVFYFELG---NIGCKVVPDCNNYRQKITSMWEPVFKPGAVDGAATYILVMVDPDAP 100
DB 61 QTIKIYTPQSDVEVSLGNQLTPTQVKARPKLWHEVEP-----SALTLLMADPDAP 111
QY 101 SRAEPQRFWRHVLVTDIKADLKGKIQGQELSAVOAPSPAHSGFHRFYOFFVYLQEGK 160
DB 112 SRSNPNRWSKHWLVGNIPGADV-----LADYVSGSPGPGTGLHRYVFLVYKQPSR 167
QY 161 VI---SLLPKENKTRGSKMDRLNRFHLGPEASTQFMNTQYQDSPTLQA 208
DB 168 IVFNETVLSRNPNGKWNPAEFVKEVGLGVPVAGNFYQAYQDYDYPVELYA 218

RESULT 5
Q7PWN1 PRELIMINARY; PRT; 214 AA.
AC Q7PWN1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000001393 (Fragment).
GN Name=ENSANGG00000011504;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -/- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAA01008984; EAA14862.1; -.
DR InterPro; IPR008914; PEBP.
DR Pfam; PF01161; PBP; 1.
DR ProDom; PD004330; PBP; 1.
FT NON TER 1
SQ SEQUENCE 214 AA; 23457 MW; A282300B473605F4 CRC64;

Query Match 20.4%; Score 246; DB 2; Length 214;
Best Local Similarity 43.7%; Pred. No. 2.2e-15;
Matches 52; Conservative 13; Mismatches 46; Indels 8; Gaps 2;

QY 84 AVDGATYILVMVDPDAPSAEPQRFWRHVLVTDIKADLKGKIQGQELSAVOAPSPPA 143
DB 86 ADSGALYTLTCDTPDAPSRKEPTYREWHHLVGNIPGADV---AQGETLSAYVSGSPQ 141
QY 144 HSGFHRFYQFFVYLQEGKVISLLPKENKT---RGSWKMDRLNRFHLGPEASTQFMNQ 198
DB 142 GTGLHRYVFLVYKQNGKLTDFEPRLNTSADNRGGFAIRKFAEYQLGPNVAGNFYQAE 200

RESULT 6
Q7PYP6 PRELIMINARY; PRT; 191 AA.
AC Q7PYP6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AgCP12373.
GN Name=agCG49709; ORFNames=ENSANGG000000017428;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PEST;
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RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008987; EAA01113.1; -.
DR InterPro; IPR001858; PBP.
DR InterPro; IPR008914; PBP.
DR Pfam; PF01161; PBP; 1.
DR ProDom; PD004330; PBP; 1.
DR PROSITE; PS01220; PBP; UNKNOWN.1.
SQ SEQUENCE 191 AA; 21956 MW; 031B661BF29D611D CRC64;

Query Match 19.6%; Score 236; DB 2; Length 191;
Best Local Similarity 36.3%; Pred. No. 1.8e-14;
Matches 60; Conservative 16; Mismatches 58; Indels 32; Gaps 5;

QY 46 LEVFYP-----ELGNI-----GCKVPCDNNYRKITSWMEPIVKFPGCAVDGATYILVMVD 96
DB 26 LHVTPGGLRVNLGNILTPTEVKHVE-----VAMPEAEPPDAYVALVLT 70
QY 97 PDAPSAEPQRTWRHVLVTDIKGADLKKGKIQGQELSAQAPSPAHSGFHRYPFVYL 156
DB 71 PDAPSTAPKRFREWHHLVNIIPGMDLAK----GDTLSDYIGAAPPKRTGLHRYVFLYR 126
QY 157 QEGKVI---SLLPKENTKRGSKWMDRFLNRFHLGPEASTQFMTQ 198
DB 127 QNERIYKESRLNRSQTGRGKSTHKFSEKYLEGLPVGAGNFFQAO 172

RESULT 7
PEBP RAT
ID PEBP RAT STANDARD; PRT; 186 AA.
AC P31044; P31045;
DT 01-JUL-1993 (Rel. 26, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Phosphatidylethanolamine-binding protein (PEBP) (HCNPPpp) (23 kDa
DE morphine-binding protein) (P23K) [Contains: Hippocampal cholinergic
DE neurostimulating peptide (HCNP)].
DE Name=Pbp; Synonyms=pebp;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RN STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=91042640; PubMed=1978248;
RA Grandy D.K., Hanneman E., Bunzow J., Shih M., Machida C.A.,
RA Bidlack J.M., Civelli O.;
RT "Purification, cloning, and tissue distribution of a 23-kDa rat
RT protein isolated by morphine affinity chromatography.";
RL Mol. Endocrinol. 4:1370-1376(1990).
[2]
SEQUENCE FROM N.A.
RN STRAIN=Wistar; TISSUE=Hippocampus;
RX MEDLINE=95364631; PubMed=7637590;
RA Tohdoh N., Tojo S., Agui H., Ojika K.;
RT "Sequence homology of rat and human HCNP precursor proteins, bovine
RT phosphatidylethanolamine-binding protein and rat 23-kDa protein
RT associated with the opioid-binding protein.";
RL Brain Res. Mol. Brain Res. 30:381-384(1995).
[3]
SEQUENCE FROM N.A.
RN STRAIN=Wistar; TISSUE=Epididymis, and Liver;
RX MEDLINE=94311839; PubMed=8037677;
RA Perry A.C.F., Hall L., Bell A.E., Jones R.;
RT "Sequence analysis of a mammalian phospholipid-binding protein from
RT testis and epididymis and its distribution between spermatozoa and
RT extracellular secretions";
RL Biochem. J. 301:235-242(1994).
[4]
SEQUENCE OF 39-55 AND 92-111.
TISSUE=Spem;
MEDLINE=92031654; PubMed=1932083;
RA Jones R., Hall L.;
RT "A 23 kDa protein from rat sperm plasma membranes shows sequence
RT similarity and phospholipid binding properties to a bovine brain
RT cytosolic protein.";
RL Biochim. Biophys. Acta 1080:78-82(1991).
[5]
SEQUENCE OF 1-11, AND ACETYLATION.
RX MEDLINE=92305945; PubMed=1611510;
RA Ojika K., Kojima S., Ueki Y., Fukushima N., Hayashi K., Yamamoto M.;
RT "Purification and structural analysis of hippocampal cholinergic
RT neurostimulating peptide.";
RL Brain Res. 572:164-171(1992).
[6]
CHARACTERIZATION.
RX MEDLINE=20086088; PubMed=10622376;
RA Ojika K., Mitake S., Tohdoh N., Appel S.H., Otsuka Y., Katada E.,
RA Matsukawa N.;
RT "Hippocampal cholinergic neurostimulating peptides (HCNP).";
RL Prog. Neurobiol. 60:37-83(2000).
[7]
CHARACTERIZATION.
RX MEDLINE=22478963; PubMed=12591138; DOI=10.1016/S0006-8993(02)04194-X;
RA Morishita M., Otsuka Y., Matsukawa N., Suzuki H., Nakazawa H.,
RA Maki M., Katou H., Ueda R., Ojika K.;
RT "Specific binding of 125I-hippocampal cholinergic neurostimulating
RT peptide (HCNP) to rat brain membranes: characterization and regional
RT distribution.";
RL Brain Res. 965:194-202(2003).
CC -1- FUNCTION: Binds ATP, opioids and phosphatidylethanolamine. Has
CC lower affinity for phosphatidylcholine and phosphatidylcholine.
CC Serine protease inhibitor which inhibits thrombin, neurotrophin and
CC chymotrypsin but not trypsin, tissue type plasminogen activator
CC and elastase (By similarity).
CC -1- FUNCTION: HCNP may be involved in the function of the presynaptic
CC cholinergic neurons of the central nervous system. HCNP increases
CC the production of choline acetyltransferase but not
CC acetylcholinesterase. Seems to be mediated by a specific receptor.
CC -1- SUBUNIT: Has a tendency to form dimers by disulfide cross-linking.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-bound forms exist.
CC -1- TISSUE SPECIFICITY: Major component of epididymal secretions and
CC sperm plasma membranes. It is present in cytosols from a variety
CC of other tissues. Highly expressed in brain.
CC -1- MISCELLANEOUS: Seems to be associated with memory and learning
CC disorder.
CC -1- SIMILARITY: Belongs to the phosphatidylethanolamine-binding
CC protein family.
CC
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CC
CC EMBL; X75253; CAA53032.1; -.
CC EMBL; X75254; CAA53033.1; -.
CC EMBL; X71873; CAA50708.1; -.
CC PIR; A36126; A36126.
CC PIR; S18358; S18358.
CC HSSP; P13696; 1B7A.
CC Rat-heart-2DPAGE; P31044; -.
CC RGD; 62017; Pbp.
CC InterPro; IPR001858; PBP.
CC InterPro; IPR008914; PBP.
CC Pfam; PF01161; PBP; 1.
CC ProDom; PD004330; PBP; 1.
CC PROSITE; PS01220; PBP; 1.
CC Acetylation; ATP-binding; Direct protein sequencing; Lipid-binding;
CC Serine protease inhibitor.
KW

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FT INIT_MET 0 0 Hippocampal cholinergic neurostimulating
FT PEPTIDE 1 11 peptide (by similarity).
FT MOD_RES 1 1 N-acetylalanine (in hippocampal
FT cholinergic neurostimulating peptide) (By
FT similarity).
FT CONFLICT 48 48 R -> G (in Ref. 4).
FT CONFLICT 53 54 SW -> TA (in Ref. 4).
FT SEQUENCE 186 AA; 20670 MW; F2D9DE82C8DD5BEB CRC64;

Query Match 19.6%; Score 235.5; DB 1; Length 186;
Best Local Similarity 36.5%; Pred. No. 1.9e-14;
Matches 57; Conservative 20; Mismatches 60; Indels 19; Gaps 5;

QY 52 ELNIGCKVVDCCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAPRQRFWR 111
DB 35 ELGKV---LTPTQVMNRPSISW-----DGLDPGKLYTLVLTDPDAPSRKDPKPREWH 84
QY 112 HMLVTDIKGADLKKGKIQQGELSAYQAPSPAHSGGHRHYOFFVYVLOGEKVIS---LLPK 167
DB 85 HFLVNMKNDISSGTV-----LSEYVSGGPPKDTGLHRYVWLVEQPLNCDPEPILSNK 140
QY 168 ENKTRGSKMDRFLNRFHLGPEASTQFMNTQYQDS 203
DB 141 SGNDRGKFVESRKKYHLGAPVAGTCFQAE-WDDS 175

RESULT 8
ANH63171 PRELIMINARY; PRT; 187 AA.
AC AAH63171;
DT 02-MAR-2004 (TEMBUREL. 27, Created)
DT 02-MAR-2004 (TEMBUREL. 27, Last sequence update)
DE Phosphatidylethanolamine binding protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Srapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2];
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary gland;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063171; ANH63171.1; -.
SQ SEQUENCE 187 AA; 20801 MW; F2BF053FE34B8056 CRC64;

Query Match 19.6%; Score 235.5; DB 2; Length 187;
Best Local Similarity 36.5%; Pred. No. 1.9e-14;

Mismatches 57; Conservative 20; Mismatches 60; Indels 19; Gaps 5;

QY 52 ELNIGCKVVDCCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAPRQRFWR 111
DB 36 ELGKV---LTPTQVMNRPSISW-----DGLDPGKLYTLVLTDPDAPSRKDPKPREWH 85
QY 112 HMLVTDIKGADLKKGKIQQGELSAYQAPSPAHSGGHRHYOFFVYVLOGEKVIS---LLPK 167
DB 86 HFLVNMKNDISSGTV-----LSEYVSGGPPKDTGLHRYVWLVEQPLNCDPEPILSNK 141
QY 168 ENKTRGSKMDRFLNRFHLGPEASTQFMNTQYQDS 203
DB 142 SGNDRGKFVESRKKYHLGAPVAGTCFQAE-WDDS 176

RESULT 9
PBPH CAEBL STANDARD; PRT; 221 AA.
AC 016264;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Phosphatidylethanolamine-binding protein homolog F40A3.3.
GN ORENAMES=F40A3.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Geisel C., Bradshaw H., Keppler D.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -/- SIMILARITY: Belongs to the phosphatidylethanolamine-binding
CC protein family.
CC -----
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CC -----
CC EMBL; AF016423; AAB65322.1; -.
CC PIR; T31721; T31721.
CC DR HSSP; P13696; 1A44.
CC DR WormPep; F40A3.3; CE10146.
CC DR InterPro; IPR001858; PBP.
CC DR InterPro; IPR008914; PEBP.
CC DR Pfam; PF01161; PBP; 1.
CC DR ProDom; PD004330; PBP; 1.
CC DR PROSITE; PS01220; PBP; 1.
CC KW Hypothetical protein; Lipid-binding.
CC SEQUENCE 221 AA; 24143 MW; 4828CC749D8B32AC CRC64;

Query Match 19.5%; Score 234.5; DB 1; Length 221;
Best Local Similarity 33.1%; Pred. No. 3e-14;
Matches 58; Conservative 16; Mismatches 60; Indels 41; Gaps 6;

QY 59 KVVVD--CNYRQKITSWMEPIVKFPGAVD-----GATYIL 92
DB 46 EVIPDVLASNPSPKVS-----VKFNSGVEANLGNLTPTQVKDTPVWKDAEPGALYTL 100
QY 93 VMVDPDAPSRAPRQRFWRHVLVTDIKGADLKKGKIQQGELSAYQAPSPAHSGGHRHYQF 152
DB 101 IKTDPPAPSRKEPTYREWHHLVNNIPGNDIAK----GDTLSYIGAGPPPKTGLHRYV 156
QY 153 FVYVLOGEKVIS-----LLPKENKTRGSKMDRFLNRFHLGPEASTQFMNTQYQD 202
DB 157 LIYVQSGRIEDAEHGRLTNTSGDKRGWKAADFVAXHKLGPVFGNLQFAE-YDD 210

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RA Matsukawa N., Tooyama I., Kimura H., Yamamoto T., Tsugu Y., Oomura Y.,
 RA Ojika K.;
 RT "Increased expression of hippocampal cholinergic neurostimulating
 RT peptide-related components and their messenger RNAs in the hippocampus
 RT of aged senescence-accelerated mice.";
 RL Neurosci 88:79-92(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Mateukawa N.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP STRAIN=C57BL/6; AND SEQUENCE OF 26-38; 62-75; 93-140 AND 157-179.
 RC STRAIN=C57BL/6;
 RX PubMed=11034991;
 RA Hengst U., Albrecht H., Hess D., Monard D.;
 RA "The phosphatidylethanolamine-binding protein is the prototype of a
 RT novel family of serine protease inhibitors";
 RL J. Biol. Chem. 276:535-540(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J, and NOD; TISSUE=Small intestine, and Thymus;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01286;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuoka H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Gough J.K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Frazer K.S.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Nunata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Whalesstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hironaka-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haeh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalish D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Binds ATP, opioids and phosphatidylethanolamine. Has
 CC lower affinity for phosphatidylinositol and phosphatidylcholine.
 CC Serine protease inhibitor which inhibits thrombin, neuropsin and
 CC chymotrypsin but not trypsin, tissue type plasminogen activator
 CC and elastase.
 CC -!- FUNCTION: HCNP may be involved in the function of the presynaptic
 CC cholinergic neurons of the central nervous system. HCNP increases
 CC the production of choline acetyltransferase but not
 CC acetylcholinesterase. Seems to be mediated by a specific receptor
 CC (by similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: HCNP is expressed in brain. Increased
 CC expression in aged senescence-accelerated mice.
 CC -!- SIMILARITY: Belongs to the phosphatidylethanolamine-binding
 CC protein family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL; U43206; AAB06983.1; -;
 DR EMBL; AF300422; AAG25635.1; -;
 DR EMBL; AB046417; BAB03276.1; -;
 DR EMBL; AK088212; BAC40214.1; -;
 DR EMBL; AK08037; BAB25424.1; -;
 DR EMBL; BC008169; AAB08169.1; -;
 DR HSSP; P30086; IBER.
 DR MGD; MGI:134408; Pbp.
 DR InterPro; IPR001858; PBP.
 DR InterPro; IPR008914; PEBP.
 DR Pfam; PF011161; PBP; 1.
 DR ProDom; PD004330; PBP; 1.
 DR PROSITE; PS01220; PBP; 1.
 KW Acetylation; ATP-binding; Direct protein sequencing; Lipid-binding;
 KW Serine protease inhibitor.
 FT INIT MET 0
 FT PEPTIDE 1 11 Hippocampal cholinergic neurostimulating
 FT MOD_RES 1 1 N-acetylalanine (in hippocampal
 FT CONFLICT 11 11 L -> F (in Ref. 5; BAB25424).
 FT CONFLICT 115 115 G -> S (in Ref. 1).
 SQ SEQUENCE 186 AA; 20699 MW; 403F1C7BCF3B611D CRC64;
 Query Match 18.7%; Score 225; DB 1; Length 186;
 Best Local Similarity 35.1%; Pred. No. 2e-13;
 Matches 53; Conservative 22; Mismatches 58; Indels 18; Gaps 4;
 QY 52 ELGNIGCKVVPDCNNYRQKITSWMEPIVKFPGVGDGATYILWVDPDAPSAEPRQRFWR 111
 DB 35 ELGKV---LTPQVNNRPSISW-----DGLDPGLYTLVTDPAKSPKDFRWH 84
 QY 112 HWLVTDIGADLKKGKIOGQELSAVQAPSPAHGSHFYQFVYLQEGKVIS----LLPK 167
 DB 85 HFLVNNKGNDISGTV----LSDYVGGSPSGTGLHRYVWLWVYEQPLSCDEPILSNK 140
 QY 168 ENKTRGSKWMDRFLNRFHLGPEASTQPMQTQ 198
 DB 141 SGDNRGKFKVETFRKKNYLNLPVAGTCYQAE 171
 RESULT 15
 ID D3 ONCVO STANDARD; PRT; 134 AA.
 AC P54188;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

05-JUL-2004 (Rel. 44, Last annotation update)
D3 protein (Fragment).
Name=D3;
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
ON Onchocercidae; Onchocerca.
NCBI_TaxID=6282;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=97045813; PubMed=8890735;
RX Erttmann K.D., Gallin M.Y.;
RA "Onchocerca volvulus: identification of cDNAs encoding a putative
RT phosphatidyl-ethanolamine-binding protein and a putative partially
processed mRNA precursor.";
RL Gene 174:203-207(1996).
CC -!- SIMILARITY: Belongs to the phosphatidylethanolamine-binding
CC protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X87989; CAA61242.1; -.
DR PIR; PC4214; PC4214.
DR HSP; P13696; IAA4.
DR InterPro; IPR001858; PBP.
DR InterPro; IPR008914; PEBP.
DR Pfam; PF01161; PBP; 1.
DR ProDom; PD004330; PBP; 1.
DR PROSITE; PS01220; PBP; 1.
FT NON TER 1
SQ SEQUENCE 134 AA; 14880 MW; AC98F5C500A251F2 CRC64;

Query Match 18.5%; Score 223; DB 1; Length 134;
Best Local Similarity 36.3%; Pred. No. 2e-13;
Matches 53; Conservative 18; Mismatches 59; Indels 16; Gaps 5;

QY 55 NIGCKVVP-DCNNYRQKITSMPEIVKFGAVDGTATYLVMDPDAPSRAEPRORFWRHW 113
Db 2 NLGNELTPTQVKNQPTKV-SW-----DAEPGALYTLVMTDPAFKNPNVFEWHHW 52

QY 114 LVTDIKGADLKKGKIQGQELSAQAPSPAHSGFHRVQFFVYLOEGKVISLLPRENKTRG 173
Db 53 LIINISGVNVSSTV---LSDYIGSGQPKGTGLHRYVFLVYKQPGSIID--TQHGGRNP 106

QY 174 SWKMDRFLNRFHLGEPPEASTQFMTON 199
Db 107 NFKVMDPFANKHHLGNPVAGNFFQAKH 132

Search completed: January 30, 2005, 17:10:02
Job time : 223 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 30, 2005, 16:52:19 ; Search time 24 Seconds

(without alignments)
894.014 Million cell updates/sec

Title: US-10-035-958-61

Perfect score: 1204

Sequence: 1 MGWTELVTAALLGLMVV.....PTLQAPGRASEPKHKTRQR 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

1: PIR.79:**

2: PIR.2:**

3: PIR.3:**

4: PIR.4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	235.5	19.6	187	2	A36126
2	234.5	19.5	221	2	T31721
3	223	18.5	134	2	PC4214
4	222	18.4	152	2	PC4216
5	218.5	18.1	186	2	S00056
6	218.5	18.1	186	2	S18358
7	210	17.4	114	2	PC4215
8	206	17.1	187	2	S46485
9	205	17.0	187	2	I53745
10	183	15.2	172	2	T27310
11	182	15.1	175	2	T52446
12	169.5	14.1	282	2	A57391
13	164	13.6	175	2	T52447
14	148.5	12.3	175	2	T07877
15	148	12.3	181	2	S68507
16	147	12.2	175	2	C84674
17	139	11.5	152	2	A44947
18	137.5	11.4	177	2	T48411
19	133	11.0	201	2	S51424
20	122.5	10.2	219	2	S18843
21	113.5	9.4	197	2	C70519
22	113	9.4	151	2	E69134
23	113	9.4	215	2	T48789
24	110.5	9.2	154	2	H97860
25	106	8.8	171	2	B70408
26	105	8.7	198	2	T11072
27	101	8.4	122	2	T52448
28	100	8.3	216	2	E84365
29	96.5	8.0	150	2	C86600

conserved hypothet
conserved hypothet
ybcL protein - Esc
probable lppc prot
conserved hypothet
hypothetical prote
conserved hypothet
conserved hypothet
glutamyl-tRNA synt
hypothetical prote
plexin A - fruit f
conserved hypothet
hypothetical prote
muscarinic acetyl
nucleur/mitotic ap
fxuD protein - Myc
conserved hypothet
conserved hypothet
hypothetical prote
hypothetical prote
phosphoadenyl-
hypothetical prote
repetin - mouse
DNA (cytosine-5-) -
lipopolysaccharide
bfpD protein - Esc
sha protein - frui
endopeptidase 2 (E
hypothetical prote
alpha-mannosidase
1-phosphatidylinos
ferroxamine recep
hypothetical prote
BEM1 protein-bindi
probable membrane
carbamoyl-phosphat
hypothetical prote
alpha-mannosidase
bacitracin synthet
hypothetical prote
probable dioxigena
ABC transporter in
hypothetical prote
SHP substrate-1 pr
hypothetical prote
biphenyl dioxigena
hypothetical prote
AMP deaminase (BC
protein-tyrosine-p
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical outer
probable periplasm
ExoI protein - Rhi
histone H1.b - gar
esterase all0992 -
follistatin-relate
conserved hypothet
hypothetical prote
hypothetical prote
catechol oxidase (
catechol oxidase (
preprotein translo
valine-tRNA ligase
probable limproted
hypothetical prote
hypothetical prote
hypothetical prote
protein F3M8.4 [i

103	71.5	5.9	649	2	T05630	hypothetical prote	176	67.5	5.6	204	2	G82589	conserved hypothet
104	71.5	5.9	725	2	D81976	probable ferric si	177	67.5	5.6	236	2	AG3072	conserved hypothet
105	71.5	5.9	774	1	ORECFA	iron(III) dicitrat	178	67.5	5.6	236	2	B98214	bbsi protein (AF17
106	71.5	5.9	1047	2	AFI912	hypothetical prote	179	67.5	5.6	277	2	B64206	hypothetical prote
107	71	5.9	283	4	FOHUE1	retrovirus-related	180	67.5	5.6	291	2	S74948	hypothetical prote
108	71	5.9	659	2	A64119	glyX protein (EC 3	181	67.5	5.6	472	2	S27878	selenium-binding p
109	71	5.9	833	1	S20387	outer membrane pro	182	67.5	5.6	516	2	E95301	hypothetical prote
110	71	5.9	833	1	T14703	FI capsule anchori	183	67.5	5.6	532	2	S27373	hypothetical prote
111	71	5.9	1004	2	B50339	outer cell wall pr	184	67.5	5.6	550	2	E90723	beta-fructofuranos
112	71	5.9	1323	2	T00037	hypothetical prote	185	67.5	5.6	550	2	E85574	probable fumarate
113	70.5	5.9	144	2	T38634	40s ribosomal prot	186	67.5	5.6	582	2	E81048	probable fumarate
114	70.5	5.9	237	2	E71128	arginase related p	187	67.5	5.6	585	2	E81048	conserved hypothet
115	70.5	5.9	423	2	B88450	protein F21H11.3 [188	67.5	5.6	596	1	S33540	hypothetical prote
116	70.5	5.9	525	2	S24791	nucleocapsid prote	189	67.5	5.6	621	1	YRNC	catechol oxidase (
117	70.5	5.9	525	2	A49277	nucleocapsid prote	190	67.5	5.6	706	2	S61717	monophenol monooxy
118	70.5	5.9	532	2	T49873	calnexin homolog -	191	67.5	5.6	1430	2	D82533	probable membrane
119	70.5	5.9	830	2	S56940	factor arrest prot	192	67	5.6	41	2	PN0155	RNA polymerase bet
120	70	5.8	306	1	JQ1395	phosphoribosylamin	193	67	5.6	114	2	S04585	RSP-24.5K protein
121	70	5.8	466	2	A40972	muscarinic acetylch	194	67	5.6	120	2	A48837	neural cell adhesi
122	70	5.8	469	2	S44655	ZK353.8 protein -	195	67	5.6	157	2	B48837	subgroup A Rous sa
123	70	5.8	485	2	T03638	hypothetical prote	196	67	5.6	158	1	Q3ECBA	subgroup A Rous sa
124	70	5.8	641	2	P82202	hypothetical prote	197	67	5.6	158	2	AF0596	conserved hypothet
125	70	5.8	784	2	H83158	Fe(III) dicitrate	198	67	5.6	158	2	D85585	conserved hypothet
126	70	5.8	1395	2	S25997	gene atpA intron 1	199	67	5.6	158	2	C90735	hypothetical prote
127	69.5	5.8	255	2	H71154	probable competenc	200	67	5.6	205	1	S33228	hypothetical prote
128	69.5	5.8	336	2	S30972	minor tail protein	201	67	5.6	274	2	D90814	ribosomal protein
129	69.5	5.8	456	2	T48291	hypothetical prote	202	67	5.6	274	2	H85673	probable beta-gluc
130	69.5	5.8	476	2	AH2115	transcription regu	203	67	5.6	311	2	C84101	beta-glucosidase (
131	69.5	5.8	525	2	S47308	gene N protein - r	204	67	5.6	330	2	G82373	hypothetical prote
132	69.5	5.8	599	2	T07037	catechol oxidase (205	67	5.6	346	2	H72237	glycyl-tRNA synthe
133	69.5	5.8	747	1	A27366	AMP deaminase (EC	206	67	5.6	361	2	T21136	hypothetical prote
134	69.5	5.8	780	2	H64830	probable membrane	207	67	5.6	367	2	D82261	hypothetical prote
135	69.5	5.8	1284	2	T50993	hypothetical prote	208	67	5.6	372	2	A52622	phoH family protei
136	69.5	5.8	2029	1	TDFPFX	protein-tyrosine-p	209	67	5.6	431	2	D75455	protein kinase (EC
137	69	5.7	106	2	E69048	conserved hypothet	210	67	5.6	465	2	B85058	5'-adenylylsulfate
138	69	5.7	235	2	D82836	hypothetical prote	211	67	5.6	474	1	JH0790	lipoprotein lipase
139	69	5.7	297	2	AB2284	hypothetical prote	212	67	5.6	505	2	S08598	hypothetical prote
140	69	5.7	403	2	T49645	late L1 52K protei	213	67	5.6	543	2	S88467	hypothetical prote
141	69	5.7	415	1	WNA052	hypothetical prote	214	67	5.6	556	2	JC5132	CD40 receptor-asso
142	69	5.7	539	2	T47404	hypothetical prote	215	67	5.6	567	2	I49272	CD40 receptor-asso
143	69	5.7	780	2	D90753	hypothetical prote	216	67	5.6	568	2	A55960	CD40 receptor-asso
144	69	5.7	80	2	B85617	hypothetical prote	217	67	5.6	678	2	T43539	spindle checkpoint
145	69	5.7	834	2	T151568	argonaute-like pro	218	67	5.6	793	2	A1750	exoribonuclease RN
146	69	5.7	892	2	T151595	hypothetical prote	219	67	5.6	812	2	T03659	phospholipase D (E
147	69	5.7	1647	2	T49412	hypothetical prote	220	67	5.6	4151	2	G70944	probable polyketid
148	69	5.7	2810	2	T22298	hypothetical prote	221	66.5	5.5	309	2	H81993	hypothetical prote
149	68.5	5.7	175	1	WCHCS	coagulogen - horse	222	66.5	5.5	410	2	A29393	hemocyanin beta-c
150	68.5	5.7	189	2	G82586	translation elonga	223	66.5	5.5	429	2	F86240	hypothetical prote
151	68.5	5.7	224	2	E75388	NADH dehydrogenase	224	66.5	5.5	495	2	G84193	Glu-tRNA amidotran
152	68.5	5.7	239	2	C84392	signal sequence pe	225	66.5	5.5	532	2	S27372	beta-fructofuranos
153	68.5	5.7	335	2	T39033	hypothetical prote	226	66.5	5.5	532	2	T79352	hypothetical prote
154	68.5	5.7	502	2	T03019	probable ribosomal	227	66.5	5.5	639	2	E72336	hypothetical prote
155	68.5	5.7	695	2	G85135	hypothetical prote	228	66.5	5.5	725	2	H81030	maioextrin glyco
156	68.5	5.7	706	2	G71004	hypothetical prote	229	66.5	5.5	790	2	T34293	hypothetical prote
157	68.5	5.7	754	2	AE0614	probable competenc	230	66.5	5.5	973	2	T35238	probable secreted
158	68.5	5.7	882	2	C83334	hypothetical prote	231	66.5	5.5	1948	2	S00485	gene 11-1 protein
159	68.5	5.7	948	2	T26417	hypothetical prote	232	66.5	5.5	2397	1	A55535	versican precursor
160	68.5	5.7	4307	2	T20721	hypothetical prote	233	66	5.5	186	2	F85044	probable M-type th
161	68	5.6	205	2	F83333	hypothetical prote	234	66	5.5	238	2	C70479	thiol-disulfide in
162	68	5.6	229	2	A49101	enolase-phosphatas	235	66	5.5	311	2	AF2353	hypothetical prote
163	68	5.6	311	2	T36739	hypothetical prote	236	66	5.5	350	2	AE2247	muconate cyclisom
164	68	5.6	415	1	WNA065	late L1 52K protei	237	66	5.5	401	2	AI2842	carbamoylphosphate
165	68	5.6	424	2	T46197	hypothetical prote	238	66	5.5	423	2	AC1068	probable membrane
166	68	5.6	475	1	LIHUL	lipoprotein lipase	239	66	5.5	456	2	B97620	hypothetical prote
167	68	5.6	603	2	T00379	KIAA0640 protein -	240	66	5.5	466	2	T41076	hypothetical prote
168	68	5.6	1075	2	D70568	hypothetical prote	241	66	5.5	493	1	D64806	hypothetical prote
169	68	5.6	1173	2	T31421	C-terminal domain-	242	66	5.5	493	2	F90720	probable proton/ol
170	68	5.6	1231	1	A48490	endo-1,4-beta-xyla	243	66	5.5	493	2	D85571	probable transport
171	68	5.6	1251	1	T34022	zonadhesin - pig	244	66	5.5	520	2	AF2750	probable transport
172	68	5.6	2476	2	CYP277	heat shock protein	245	66	5.5	547	2	E97531	acyl-CoA dehydroge
173	67.5	5.6	157	1	E70080	conserved hypothet	246	66	5.5	635	2	E71733	probable acyl-CoA
174	67.5	5.6	168	2	E70080	conserved hypothet	247	66	5.5	638	2	T36309	threonine-tRNA lig
175	67.5	5.6	195	1	B27257	coagulogen II prec	248	66	5.5	692	2	AD1857	hypothetical prote

249	66	5.5	775	2	S67920	DNA-directed DNA p	322	64.5	5.4	258	2	G97655	hypothetical prote
250	66	5.5	776	2	B96666	protein F22C12.6 [323	64.5	5.4	300	1	NDBPT7	exodeoxyribonuclea
251	66	5.5	795	2	T43447	hypothetical prote	324	64.5	5.4	309	2	E83243	probable transcript
252	66	5.5	1042	2	S76045	hypothetical prote	325	64.5	5.4	319	2	D90482	dehydrogenase, pro
253	66	5.5	1078	2	D87647	hypothetical prote	326	64.5	5.4	330	2	AF0842	multidrug resistan
254	66	5.5	1095	2	B83471	probable pyruvate	327	64.5	5.4	336	2	H72224	hypothetical prote
255	66	5.5	1520	2	T30820	carbamoyl-phosphat	328	64.5	5.4	407	2	C71055	probable RNA methy
256	66	5.5	1524	2	T30518	acetyl-CoA carboxy	329	64.5	5.4	439	2	S25483	ribulose-bisphosph
257	66	5.5	2089	1	A48757	chondroitin sulfat	330	64.5	5.4	442	2	S20908	tubulin beta chain
258	66	5.5	2325	2	A61208	polyketide synthas	331	64.5	5.4	445	2	A60488	histidine-rich gly
259	66	5.5	2478	2	AH2140	genome polyprotein	332	64.5	5.4	447	2	AF1751	RNA polymerase sig
260	66	5.5	3068	1	A44062	probable membrane	333	64.5	5.4	454	2	S75610	UDP-N-acetylmutamo
261	65.5	5.4	122	2	AB0019	Shaking-B neural p	334	64.5	5.4	462	2	G82094	sodium-translocati
262	65.5	5.4	122	2	JY0441	heat shock protein	335	64.5	5.4	471	2	AB2266	trigger factor [im
263	65.5	5.4	159	1	CNP279	coagulogen precurs	336	64.5	5.4	512	2	T45686	receptor-like prot
264	65.5	5.4	195	1	WCHCA	hypothetical prote	337	64.5	5.4	540	2	H72076	methionine-tRNA li
265	65.5	5.4	266	2	T20142	hypothetical prote	338	64.5	5.4	551	2	H72117	hypothetical prote
266	65.5	5.4	279	2	T47120	pantoate-beta-alan	339	64.5	5.4	558	2	S38614	hypothetical prote
267	65.5	5.4	282	2	H71547	probable disulfide	340	64.5	5.4	612	2	H82022	glutamine-fructose
268	65.5	5.4	368	2	G87637	hypothetical prote	341	64.5	5.4	613	2	S48557	hypothetical prote
269	65.5	5.4	375	2	H90786	hypothetical prote	342	64.5	5.4	617	2	G64972	yegA protein precu
270	65.5	5.4	375	2	H85646	hypothetical prote	343	64.5	5.4	692	2	C55926	DNA binding protei
271	65.5	5.4	375	2	H64843	ycoD protein - Esc	344	64.5	5.4	753	2	JC2099	glutinin, high mol
272	65.5	5.4	409	2	H69506	probable acyl-CoA	345	64.5	5.4	786	2	T49414	related to ampl p
273	65.5	5.4	433	2	A83691	hypothetical prote	346	64.5	5.4	812	2	T03402	probable phospholi
274	65.5	5.4	435	2	B86149	TiN6.17 protein -	347	64.5	5.4	830	2	T49270	receptor protein k
275	65.5	5.4	448	2	C83793	hypothetical prote	348	64.5	5.4	1038	1	S03632	Na+/K+-exchangin
276	65.5	5.4	456	2	C70481	translation initia	349	64.5	5.4	1056	2	T02930	lysine-ketoglutar
277	65.5	5.4	459	2	B44498	radial spoke prote	350	64.5	5.4	1173	2	T51440	alpha-mannosidase
278	65.5	5.4	469	2	S44620	C50C3.1 protein -	351	64.5	5.4	1176	2	JN0583	myosin-light-chain
279	65.5	5.4	542	2	I39540	chitinase [EC 3.2.	352	64.5	5.4	1221	2	T52347	disease resistanc
280	65.5	5.4	562	2	B70609	hypothetical prote	353	64.5	5.4	2819	2	A90551	conserved hypothet
281	65.5	5.4	664	2	F83376	conserved hypothet	354	64	5.3	200	2	AC0522	hypothetical prote
282	65.5	5.4	709	2	E75601	probable transposa	355	64	5.3	263	2	AC0522	probable secreted
283	65.5	5.4	837	2	D69171	intracellular prot	356	64	5.3	385	2	T22822	hypothetical prote
284	65.5	5.4	892	2	AH2736	DNA topoisomerase	357	64	5.3	397	2	F72072	hypothetical prote
285	65.5	5.4	882	2	F97517	hypothetical prote	358	64	5.3	397	2	C86552	probable transamin
286	65.5	5.4	1285	2	T03302	pitriylisin (EC 3.4	359	64	5.3	442	2	G70158	aspartate aminotra
287	65.5	5.4	3795	2	T00831	hypothetical prote	360	64	5.3	445	2	D86620	UDP-N-acetylglucos
288	65	5.4	231	2	B71261	probable spoIIJ-a	361	64	5.3	445	2	T32004	phosphohikimate v
289	65	5.4	255	2	D70635	hypothetical prote	362	64	5.3	502	2	C735910	phosphohikimate v
290	65	5.4	306	2	S51361	folistatin-relate	363	64	5.3	503	2	AE1061	probable carboxyle
291	65	5.4	359	2	B85566	probable ATP-bind	364	64	5.3	532	2	T46649	leucyl aminopeptid
292	65	5.4	359	2	B64801	ybeZ protein - Esc	365	64	5.3	532	2	T49181	1,3-beta-glucan sy
293	65	5.4	359	2	B90716	probable ATP-bind	366	64	5.3	611	2	AC2094	cyclophylin-like p
294	65	5.4	389	2	D40785	hypothetical 46K p	367	64	5.3	612	2	C64535	two-component resp
295	65	5.4	459	1	B41858	hypothetical 46K p	368	64	5.3	641	2	S64064	threonine-tRNA lig
296	65	5.4	559	2	C87307	biphenyl dioxygena	369	64	5.3	645	2	A75390	probable membrane
297	65	5.4	614	2	E96568	hypothetical prote	370	64	5.3	662	2	C97507	NADH2 dehydrogenas
298	65	5.4	622	2	A40144	unknown protein, 1	371	64	5.3	662	2	AC9725	hypothetical prote
299	65	5.4	629	2	T15945	prolactin receptor	372	64	5.3	664	2	G86663	2',3'-cyclic-nucle
300	65	5.4	635	2	H97736	hypothetical prote	373	64	5.3	787	2	C75068	hypothetical prote
301	65	5.4	672	2	T50259	threonine-tRNA lig	374	64	5.3	920	2	T26650	probable beta-gala
302	65	5.4	697	2	T00267	probable serine/th	375	64	5.3	1065	2	A70797	hypothetical prote
303	65	5.4	733	2	T49679	hypothetical prote	376	64	5.3	1146	2	S46837	hypothetical prote
304	65	5.4	773	2	T46283	probable branching	377	64	5.3	1147	1	MWAXIB	hypothetical prote
305	65	5.4	1066	2	F71100	hypothetical prote	378	63.5	5.3	175	1	WCHCJ	myosin heavy chain
306	65	5.4	1087	1	S41797	isoleucine-tRNA li	379	63.5	5.3	231	2	C97552	coagulogen I - hor
307	65	5.4	1177	2	AD0438	cellulose 1,4-beta	380	63.5	5.3	231	2	AD2772	hypothetical prote
308	65	5.4	1284	2	G86145	probable exported	381	63.5	5.3	260	2	AH2158	hypothetical prote
309	65	5.4	1291	1	A28334	F22L4.6 protein -	382	63.5	5.3	268	2	S76063	hypothetical prote
310	65	5.4	1308	2	B32494	protein-tyrosine-p	383	63.5	5.3	308	2	T49920	hypothetical prote
311	65	5.4	1352	2	G84473	transposable eleme	384	63.5	5.3	390	2	F65048	multidrug resistan
312	65	5.4	1424	2	T03851	hypothetical prote	385	63.5	5.3	414	2	AH1662	sugar ABC transpor
313	65	5.4	1434	2	T30172	thyroid hormone re	386	63.5	5.3	440	2	A56693	receptor protein k
314	65	5.4	1434	2	S09811	transmembrane prot	387	63.5	5.3	482	2	S10180	bactericidal perme
315	65	5.4	2241	2	T13719	hypothetical prote	388	63.5	5.3	486	2	T27548	hypothetical prote
316	64.5	5.4	416	2	AL57321	calo protein - fru	389	63.5	5.3	496	2	AB2219	hypothetical prote
317	64.5	5.4	128	1	T17873	E48 antigen precu	390	63.5	5.3	499	2	JC2062	transforming growt
318	64.5	5.4	152	2	CTSHP	hypothetical prote	391	63.5	5.3	503	2	A49432	activin receptor-1
319	64.5	5.4	212	1	CTSHP	corticotropin / li	392	63.5	5.3	503	2	JC2061	transforming growt
320	64.5	5.4	232	2	E90592	hypothetical prote	393	63.5	5.3	525	2	H70982	probable fadd7 pro
321	64.5	5.4	253	2	A81269	pseudouridyate sy	394	63.5	5.3	527	2	T02128	beta-glucosidase h
322	64.5	5.4	258	2	AE2879	conserved hypothet							

395	63.5	5.3	597	1	P21VTV	RNA-directed RNA p	468	62.5	5.2	210	2	D87724	protein F37F2.1 li
396	63.5	5.3	612	2	B81246	glutamine-fructose	469	62.5	5.2	210	2	T33051	hypothetical prote
397	63.5	5.3	663	2	S32825	arachidonate 12-li	470	62.5	5.2	244	2	T12458	hypothetical prote
398	63.5	5.3	732	2	S23001	trai protein - Esc	471	62.5	5.2	261	2	C72128	hypothetical prote
399	63.5	5.3	796	2	G82582	bifunctional penic	472	62.5	5.2	261	2	F86494	hypothetical prote
400	63.5	5.3	831	2	S50163	nitrate reductase	473	62.5	5.2	269	2	AF0138	probable exported
401	63.5	5.3	889	2	H96606	hypothetical prote	474	62.5	5.2	278	2	G81139	hypothetical prote
402	63.5	5.3	909	2	T00009	probable primase (475	62.5	5.2	283	2	T49546	hypothetical prote
403	63.5	5.3	934	2	T08418	protein kinase (RC	476	62.5	5.2	288	2	T04894	hypothetical prote
404	63.5	5.3	945	2	A64714	helicase - Helicob	477	62.5	5.2	295	2	A48906	glucose-1-phosphat
405	63.5	5.3	1192	2	T17255	hypothetical prote	478	62.5	5.2	307	2	T19906	hypothetical prote
406	63.5	5.3	1861	2	T13845	microtubule-associ	479	62.5	5.2	309	1	E65112	hypothetical 34.6
407	63	5.3	140	1	S57774	thioredoxin m prec	480	62.5	5.2	309	2	E85985	hypothetical prote
408	63	5.2	175	2	E90877	probable copper/zi	481	62.5	5.2	309	2	B91140	hypothetical prote
409	63	5.2	246	2	S46747	hypothetical prote	482	62.5	5.2	319	2	B90958	probable plasmid p
410	63	5.2	247	2	T50286	hypothetical prote	483	62.5	5.2	319	2	C85806	probable plasmid p
411	63	5.2	255	2	JQ0320	hypothetical 24.7K	484	62.5	5.2	328	2	A95011	conserved hypothet
412	63	5.2	267	2	T47288	hypothetical prote	485	62.5	5.2	328	2	D97882	conserved hypothet
413	63	5.2	278	2	D63208	protein F22G5.34 (486	62.5	5.2	344	2	JX0366	cysteine endopepti
414	63	5.2	328	2	E85842	probable superoxid	487	62.5	5.2	361	1	A61648	translation releas
415	63	5.2	330	2	A72534	hypothetical prote	488	62.5	5.2	361	2	AB2462	hypothetical prote
416	63	5.2	341	2	E81779	iron (III) dicitra	489	62.5	5.2	365	2	B90250	oxidoreductase, pr
417	63	5.2	349	2	AF1714	ribonucleoside-dip	490	62.5	5.2	370	2	T40131	hypothetical prote
418	63	5.2	350	2	AC2375	hypothetical prote	491	62.5	5.2	376	2	AC0470	probable lipopolys
419	63	5.2	355	2	A12867	endo-1,4-beta-xyla	492	62.5	5.2	389	2	A12230	mannose-1-phosphat
420	63	5.2	365	2	E97644	endo-1,4-beta-xyla	493	62.5	5.2	390	2	F85916	multidrug resistan
421	63	5.2	426	2	S44953	lmbP protein - Str	494	62.5	5.2	390	2	C91072	sugar ABC transpor
422	63	5.2	435	2	S52203	vsl-1 protein - to	495	62.5	5.2	414	2	AB1291	epithelial zinc-fi
423	63	5.2	464	2	T38356	septin homolog spn	496	62.5	5.2	445	2	T49556	probable AP2 domai
424	63	5.2	474	2	S77650	probable transposa	497	62.5	5.2	464	2	C84686	cytochrome P450 4A
425	63	5.2	478	1	S60754	transcription fact	498	62.5	5.2	504	1	A32965	hypothetical prote
426	63	5.2	478	2	S18158	lipoprotein lipase	499	62.5	5.2	506	2	H70928	hypothetical prote
427	63	5.2	527	2	G85760	hypothetical prote	500	62.5	5.2	522	2	F70143	hypothetical prote
428	63	5.2	527	2	H90858	hypothetical prote	501	62.5	5.2	537	2	T04745	hypothetical prote
429	63	5.2	529	2	T35831	probable D-3-phosp	502	62.5	5.2	558	2	A13394	metal dependent by
430	63	5.2	529	2	G82759	hypothetical prote	503	62.5	5.2	559	2	G89931	DNA repair protein
431	63	5.2	530	2	JN0597	calnexin-like prot	504	62.5	5.2	586	2	B84271	glutamyl-tRNA sync
432	63	5.2	532	1	IFBY	beta-fructofuranos	505	62.5	5.2	589	2	F86202	hypothetical prote
433	63	5.2	545	2	T02079	probable carbonate	506	62.5	5.2	602	2	G83388	probable binding p
434	63	5.2	549	2	S04845	lg heavy chain pre	507	62.5	5.2	606	2	E84889	hypothetical prote
435	63	5.2	582	2	S57722	slf-1 protein - Ca	508	62.5	5.2	607	2	E71518	prolactin receptor
436	63	5.2	589	2	E97376	sulfite reductase	509	62.5	5.2	616	2	A30304	cell division cont
437	63	5.2	589	2	AD2594	hypothetical prote	510	62.5	5.2	637	2	A45777	hypothetical prote
438	63	5.2	606	2	AF2903	GTP-binding tyrosi	511	62.5	5.2	688	2	S65241	hypothetical prote
439	63	5.2	606	2	H97678	hypothetical prote	512	62.5	5.2	844	2	T37690	ubiquitin thiolest
440	63	5.2	612	2	T38717	threonine-CRNA lig	513	62.5	5.2	858	2	S68227	phosphoenolpyruvat
441	63	5.2	616	2	T19563	probable GRP-bind	514	62.5	5.2	898	2	P97993	probable disease r
442	63	5.2	629	2	T19563	hypothetical prote	515	62.5	5.2	905	2	T08475	1-phosphatidylinos
443	63	5.2	644	2	S65302	hypothetical prote	516	62.5	5.2	1043	2	T43502	sucrose-phosphate
444	63	5.2	648	2	A83792	acetyl-CoA synthet	517	62.5	5.2	1068	1	JQ1329	neural cell adhesi
445	63	5.2	651	2	T40459	hypothetical lysin	518	62.5	5.2	1115	1	IJMSNL	hypothetical prote
446	63	5.2	657	2	A54278	DNA-binding protei	519	62.5	5.2	1254	2	S46636	probable tail-host
447	63	5.2	683	2	CA9784	phycobilisome anch	520	62.5	5.2	1276	2	T09204	probable tail-host
448	63	5.2	738	2	C84700	hypothetical prote	521	62.5	5.2	1291	2	T09273	M polypeptide prec
449	63	5.2	748	1	S74389	phytochrome phy -	522	62.5	5.2	1551	1	A43364	hypothetical prote
450	63	5.2	753	2	AE0187	probable iron-side	523	62.5	5.2	1554	2	C72647	3-dehydroquinatate s
451	63	5.2	778	2	B71164	hypothetical prote	524	62.5	5.2	1603	1	BVASA1	hypothetical prote
452	63	5.2	966	2	D96862	Na+/K+-exchanging	525	62.5	5.2	2215	2	T16871	probable non-ribos
453	63	5.2	1004	2	JH0470	Ca(2+)-sensing rec	526	62.5	5.2	2352	2	C83229	conserved hypothet
454	63	5.2	1085	2	S40476	C28A5.1 protein (c	527	62	5.1	149	2	F83483	uncharacterized co
455	63	5.2	1223	2	S43579	proline dehydrogen	528	62	5.1	165	2	E97317	Pe-tbx-2 protein -
456	63	5.2	1274	2	B81779	conserved hypothet	529	62	5.1	182	2	D56530	P II nitrogen sens
457	63	5.2	1438	2	AI0093	patched protein -	530	62	5.1	196	2	D85024	hypothetical prote
458	63	5.2	1442	2	T18538	anucleate primary	531	62	5.1	241	2	C70549	hypothetical prote
459	63	5.2	1676	2	A56508	gramicidin S synth	532	62	5.1	250	2	D75364	hypothetical prote
460	63	5.2	4450	2	JX0340	gramicidin S synth	533	62	5.1	277	2	T43099	hypothetical prote
461	63	5.2	4452	1	YGBSG2	conserved hypothet	534	62	5.1	281	2	JCS284	carboxyl reductase
462	62.5	5.2	133	2	AGB3048	hypothetical prote	535	62	5.1	284	2	T00809	probable esterase
463	62.5	5.2	149	2	D98237	heat shock protein	536	62	5.1	284	2	AB0521	AmpE protein [lmpo
464	62.5	5.2	149	2	T04171	heat shock protein	537	62	5.1	301	2	A70039	ABC transporter (A
465	62.5	5.2	156	2	S71566	heme exporter prot	538	62	5.1	301	2	S75554	tRNA delta-2-isope
466	62.5	5.2	205	2	AD0788	heme exporter prot	539	62	5.1	306	2	A48993	protein-tyrosine-p
467	62.5	5.2	205	2	AC0960	heme exporter prot	540	62	5.1	314	2	T45077	ornithine carbamoy

541	62	5.1	318	2	A86750	hypothetical prote	614	61.5	5.1	362	2	B83542	hypothetical prote
542	62	5.1	321	2	A12679	conserved hypotet	615	61.5	5.1	405	2	C90194	hypothetical prote
543	62	5.1	321	2	G7461	hypothetical prote	616	61.5	5.1	453	2	D40630	phosphomannomutase
544	62	5.1	332	2	T20231	1,3-beta-glucanase	617	61.5	5.1	469	2	B81050	hypothetical prote
545	62	5.1	334	2	A82443	D-alanine-D-alanin	618	61.5	5.1	469	2	B81826	probable integral
546	62	5.1	346	2	S72222	ferredoxin-NADP re	619	61.5	5.1	490	2	F87443	conserved hypotet
547	62	5.1	349	2	A81344	ribonucleoside-dip	620	61.5	5.1	505	2	S76722	UDP-N-acetylmuramo
548	62	5.1	352	2	AC1943	periplasmic phosph	621	61.5	5.1	507	2	T20293	hypothetical prote
549	62	5.1	352	2	S76078	streptogramin lyas	622	61.5	5.1	520	2	S72324	hypothetical prote
550	62	5.1	361	2	A80584	PhoH-like ATP-bind	623	61.5	5.1	535	2	AE3202	hypothetical prote
551	62	5.1	368	2	AC2840	ABC transporter, s	624	61.5	5.1	544	2	AF2248	hypothetical prote
552	62	5.1	368	2	E97617	hypothetical prote	625	61.5	5.1	561	2	JE0158	hypothetical prote
553	62	5.1	381	2	B87470	hypothetical prote	626	61.5	5.1	563	2	B82579	peptide synthase X
554	62	5.1	405	2	A35620	coenzyme F420 hydr	627	61.5	5.1	566	2	T15866	hypothetical prote
555	62	5.1	412	2	I46421	thymidine-binding	628	61.5	5.1	577	2	AE1697	two-component sens
556	62	5.1	436	2	JC1497	alpha-amino-epsilo	629	61.5	5.1	578	2	AG0119	probable OmpA-fami
557	62	5.1	440	2	T20092	hypothetical prote	630	61.5	5.1	660	1	ALBS	alpha-amylase (SC
558	62	5.1	456	2	B55239	phosphomannomutase	631	61.5	5.1	672	2	B81242	conserved hypotet
559	62	5.1	456	2	C30983	phosphomannomutase	632	61.5	5.1	693	2	C83821	glycyl-tRNA synthe
560	62	5.1	456	2	F85828	phosphomannomutase	633	61.5	5.1	699	2	A70300	translation elonga
561	62	5.1	460	2	S09508	muscarinic acetyl	634	61.5	5.1	728	2	D86233	hypothetical prote
562	62	5.1	487	2	A11146	hypothetical cell	635	61.5	5.1	775	2	S35543	DNA-directed DNA p
563	62	5.1	491	2	T16691	hypothetical prote	636	61.5	5.1	822	2	S56823	probable membrane
564	62	5.1	503	2	AP2029	hypothetical prote	637	61.5	5.1	858	2	S30571	DNA topoisomerase
565	62	5.1	504	2	S17248	regulatory protein	638	61.5	5.1	864	2	T42556	tegument protein 1
566	62	5.1	509	2	JC5288	SHP substrate-1 pr	639	61.5	5.1	872	1	TNBEH	97K alpha trans-in
567	62	5.1	511	2	AG0636	periplasmic glucan	640	61.5	5.1	883	2	AE0207	conserved hypotet
568	62	5.1	513	2	B96524	hypothetical prote	641	61.5	5.1	902	2	C83964	cation-transportin
569	62	5.1	521	2	T27996	hypothetical prote	642	61.5	5.1	906	2	T28034	hypothetical prote
570	62	5.1	542	2	E86628	phophage psi prote	643	61.5	5.1	959	1	B71405	probable kinesin -
571	62	5.1	551	2	C86506	methionyl-tRNA syn	644	61.5	5.1	1034	2	T17458	chromosome condens
572	62	5.1	551	2	H81552	transporth ATP-bind	645	61.5	5.1	1040	1	A38306	alpha-mannosidase
573	62	5.1	573	2	AB0611	probable sugar tra	646	61.5	5.1	1062	2	T46444	hypothetical prote
574	62	5.1	588	2	T48766	AMP deaminase homo	647	61.5	5.1	1842	2	T43409	probable fatty-aci
575	62	5.1	600	2	T01259	hypothetical prote	648	61.5	5.1	1842	2	T38781	fatty acid synthas
576	62	5.1	640	2	S75175	hypothetical prote	649	61.5	5.1	2077	1	WZB24	240K tegument prot
577	62	5.1	650	2	AB2004	hypothetical prote	650	61.5	5.1	2078	2	T09326	tegument protein -
578	62	5.1	710	2	S43360	conserved hypotet	651	61.5	5.1	2123	2	S55089	genome polyprotein
579	62	5.1	756	2	803005	multicystatin - po	652	61.5	5.1	2290	1	GNNYE	probable acetyl-Co
580	62	5.1	798	2	F50479	neurofilament medi	653	61.5	5.1	2549	2	S45340	FKBP-rapamycin-ass
581	62	5.1	822	2	F86812	phosphoketolase [i	654	61.5	5.1	2643	2	T29149	hypothetical prote
582	62	5.1	849	1	UYPVAD	noncapsid protein	655	61.5	5.1	4848	2	T30289	hypothetical prote
583	62	5.1	962	2	T51924	daf-18 protein - C	656	61	5.1	118	1	HRTHM	pristinamycin I sy
584	62	5.1	965	2	T32574	hypothetical prote	657	61	5.1	159	2	S72544	myohemerythrin [va
585	62	5.1	1021	2	T08601	hypothetical prote	658	61	5.1	161	2	E98102	heat shock protein
586	62	5.1	1063	2	E96662	hypothetical prote	659	61	5.1	161	2	D95238	hypothetical prote
587	62	5.1	1130	1	TVHUA	protein-tyrosine k	660	61	5.1	171	2	B89865	PTS system, IIA co
588	62	5.1	1199	2	T47442	disease resistance	661	61	5.1	183	2	B64547	conserved hypotet
589	62	5.1	1221	2	T23472	hypothetical prote	662	61	5.1	183	2	A71962	hypothetical prote
590	62	5.1	1228	2	T18897	hypothetical prote	663	61	5.1	205	2	T34724	probable membrane
591	62	5.1	1276	2	F83086	hypothetical prote	664	61	5.1	236	2	B90086	hypothetical prote
592	62	5.1	1335	2	JQ1258	RNA-directed RNA p	665	61	5.1	244	2	JE0170	dnaj heat shock pr
593	62	5.1	1413	2	D88844	protein ZK792.1 [i	666	61	5.1	247	2	H69493	phosphoesterase-re
594	62	5.1	1701	2	T09127	probable erythrocy	667	61	5.1	261	2	JQ0319	hypothetical 27K p
595	62	5.1	1816	2	F83901	hypothetical prote	668	61	5.1	281	2	G75430	pantoate-beta-alan
596	62	5.1	1956	2	T00051	hypothetical prote	669	61	5.1	284	2	T29001	hypothetical prote
597	62	5.1	2039	2	T15347	ankyrin-related un	670	61	5.1	286	2	T04268	hypothetical prote
598	62	5.1	2439	1	A54794	deyin heavy chain	671	61	5.1	296	2	D88969	hypothetical prote
599	61.5	5.1	144	2	AC2130	hypothetical prote	672	61	5.1	297	2	H90601	protein F15811.9 [
600	61.5	5.1	188	2	E97104	phospholipase D fa	673	61	5.1	297	2	B86161	DNA polymerase i (
601	61.5	5.1	194	2	G81726	conserved hypotet	674	61	5.1	299	2	A11208	Fl003.14 protein -
602	62	5.1	215	2	S30169	alkylmercury lyase	675	61	5.1	301	2	F83653	metal binding prot
603	61.5	5.1	228	2	D90626	cytochrome c oxida	676	61	5.1	303	2	B83164	oligopeptide ABC t
604	61.5	5.1	243	2	B82979	hypothetical prote	677	61	5.1	333	2	A75365	hypothetical prote
605	61.5	5.1	270	2	E64561	DNA processing cha	678	61	5.1	341	2	S37438	conserved hypotet
606	61.5	5.1	272	2	C75291	guanylate kinase -	679	61	5.1	351	1	MNXRRW	transposase Stre
607	61.5	5.1	282	2	AC2047	hypothetical prote	680	61	5.1	351	2	I51157	nonstructural prot
608	61.5	5.1	285	2	T22722	hypothetical prote	681	61	5.1	355	2	AG0319	major histocompati
609	61.5	5.1	299	2	F87415	glycyl-tRNA synthe	682	61	5.1	370	2	B86175	conserved hypotet
610	61.5	5.1	321	2	T07043	probable epoxide h	683	61	5.1	381	2	C87250	protein F1919.21
611	61.5	5.1	322	2	B96014	probable sugar upt	684	61	5.1	385	2	B8175	dnaj protein limpo
612	61.5	5.1	356	2	G86078	frv operon protein	685	61	5.1	393	2	S59383	probable membrane
613	61.5	5.1	356	2	H91231	frv operon protein	686	61	5.1	414	2	H90905	probable exonuclea
										414	2	G85711	

687	61	5.1	456	2	H85830	phosphomannomutase	760	60.5	5.0	410	2	AD1074	conserved hypotet
688	61	5.1	456	2	E90985	phosphomannomutase	761	60.5	5.0	416	2	AG0198	lipoprotein releas
689	61	5.1	456	2	T33622	hypothetical prote	762	60.5	5.0	422	2	S71243	phosphoadenyl-su
690	61	5.1	466	2	B82482	alpha-amylase VCAO	763	60.5	5.0	424	2	C82516	type I restriction
691	61	5.1	475	1	YXUM	citrate (si)-synth	764	60.5	5.0	433	2	S31436	Ig upsilon chain -
692	61	5.1	475	1	WZBEM4	gene 17 protein -	765	60.5	5.0	450	2	AI1299	signal recognition
693	61	5.1	492	2	G70899	probable monooxyge	766	60.5	5.0	458	2	T49106	PRH26 protein - Ar
694	61	5.1	518	2	T20908	hypothetical prote	767	60.5	5.0	468	2	AH2665	hypothetical prote
695	61	5.1	520	1	S03188	cholesterol monoox	768	60.5	5.0	468	2	G97447	met-10+ protein -
696	61	5.1	533	2	JC7985	brain-specific CUB	769	60.5	5.0	475	2	JC4255	acute myeloid leuk
697	61	5.1	536	2	D83622	arylsulfatase PA01	770	60.5	5.0	480	2	S57842	hypothetical prote
698	61	5.1	537	2	F90465	medium-chain-fatty	771	60.5	5.0	495	2	AD2275	monooxygenase-rela
699	61	5.1	544	2	AD1979	permease protein o	772	60.5	5.0	506	2	C81704	probable membrane
700	61	5.1	545	1	I48951	oncofetal antigen	773	60.5	5.0	518	2	H64775	hypothetical prote
701	61	5.1	549	1	A24436	alpha-amylase (EC	774	60.5	5.0	518	2	F90692	hypothetical prote
702	61	5.1	561	2	AE2543	hypothetical prote	775	60.5	5.0	518	2	B85543	beta-glucosidase h
703	61	5.1	597	2	T51889	related to clathri	776	60.5	5.0	520	2	T02127	hypothetical prote
704	61	5.1	623	2	S68963	phosphoprotein pho	777	60.5	5.0	524	2	C69297	acetyl-CoA decarbo
705	61	5.1	639	2	T13151	adaptor protein CM	778	60.5	5.0	525	1	JU0272	nucleocapsid prote
706	61	5.1	641	2	T03095	homeoprotein Sail	779	60.5	5.0	538	2	A83013	conserved hypotet
707	61	5.1	642	2	F84172	ABC transport prot	780	60.5	5.0	538	2	AG2902	conserved hypotet
708	61	5.1	673	2	AG0471	ATP-dependent DNA	781	60.5	5.0	545	2	F95325	probable arylsulfa
709	61	5.1	706	2	A48752	B-cell CLL/lymphom	782	60.5	5.0	550	2	H97677	hypothetical prote
710	61	5.1	725	1	P21VBS	RNA-directed RNA p	783	60.5	5.0	564	2	T30021	alpha-amylase - fi
711	61	5.1	737	2	C81724	1,4-alpha-glucan b	784	60.5	5.0	575	2	T41173	hypothetical prote
712	61	5.1	738	2	A17462	probable glucan br	785	60.5	5.0	587	2	A55976	cellulose 1,4-beta
713	61	5.1	755	2	B75288	hypothetical prote	786	60.5	5.0	596	2	A55976	gene ND1 intron 4
714	61	5.1	769	2	E90158	AAA family AFase	787	60.5	5.0	603	2	S06059	ABC transporter AT
715	61	5.1	803	2	T46179	hypothetical prote	788	60.5	5.0	626	2	AI3310	probable lipopolys
716	61	5.1	808	2	T04092	phospholipase D (E	789	60.5	5.0	660	2	AB0794	EMP70 protein prec
717	61	5.1	837	2	T23946	hypothetical prote	790	60.5	5.0	667	2	S64915	peroxidase (EC 1.1
718	61	5.1	842	2	S18462	glycoprotein H pre	791	60.5	5.0	687	2	T09051	translation elonga
719	61	5.1	932	2	JC5953	inter-alpha-inhibi	792	60.5	5.0	690	2	S28222	hypothetical prote
720	61	5.1	1018	1	GNWXG7	genome polyprotein	793	60.5	5.0	733	2	E69007	hypothetical prote
721	61	5.1	1020	2	A34474	Na+/K+-exchanging	794	60.5	5.0	754	2	E69745	phytochrome - whis
722	61	5.1	1020	2	B24639	Na+/K+-exchanging	795	60.5	5.0	773	2	T00554	glutenin, high-mol
723	61	5.1	1023	2	A59431	KIAA0013 protein (796	60.5	5.0	794	2	S37158	hypothetical prote
724	61	5.1	1138	2	S64484	phosphatidylserine	797	60.5	5.0	815	2	JN0689	DNA-binding protei
725	61	5.1	1138	2	T24635	hypothetical prote	798	60.5	5.0	827	2	S07114	probable membrane
726	61	5.1	1225	2	C84530	hypothetical prote	799	60.5	5.0	849	2	S61962	lipoxigenase (EC 1
727	61	5.1	1248	2	B96827	hypothetical prote	800	60.5	5.0	864	2	T05945	hypothetical prote
728	61	5.1	1279	2	T18312	hypothetical prote	801	60.5	5.0	865	2	AC1966	probable ATP-depen
729	61	5.1	1670	2	S71551	DNA-directed DNA p	802	60.5	5.0	872	2	H55564	formyltetrahydrofo
730	61	5.1	1876	2	T28627	vitellogenin - Rip	803	60.5	5.0	902	2	A00560	probable retrolele
731	61	5.1	2078	2	T25400	hypothetical prote	804	60.5	5.0	949	2	D84487	plectin isoform pl
732	61	5.1	6805	2	S20901	titin - rabbit (fr	805	60.5	5.0	964	2	D59404	genome polyprotein
733	60.5	5.0	143	2	F75475	3-dehydroquinate d	806	60.5	5.0	980	2	A38523	formate dehydrogen
734	60.5	5.0	180	2	T12493	hypothetical prote	807	60.5	5.0	985	2	E69850	kiotro protein - r
735	60.5	5.0	182	2	AG0040	single-strand bind	808	60.5	5.0	1014	2	JE0333	carbamoylphosphate
736	60.5	5.0	198	2	B83598	conserved hypotet	809	60.5	5.0	1073	2	E83051	carbamoyl-phosphat
737	60.5	5.0	200	2	D83997	hypothetical prote	810	60.5	5.0	1076	2	D82083	probable recB prot
738	60.5	5.0	208	2	S03615	glutathione transf	811	60.5	5.0	1094	2	C70612	inner layer protei
739	60.5	5.0	208	2	S76097	hypothetical prote	812	60.5	5.0	1159	1	A44280	adenosine deaminas
740	60.5	5.0	231	2	AC2213	hypothetical prote	813	60.5	5.0	1226	1	S65593	hypothetical prote
741	60.5	5.0	244	2	S76301	hypothetical prote	814	60.5	5.0	1253	2	T46248	orf la protein - l
742	60.5	5.0	255	2	E70166	exodeoxyribonuclea	815	60.5	5.0	2396	2	B36861	cell wall alpha-gl
743	60.5	5.0	259	2	AG3607	probable hydroxlas	816	60.5	5.0	2410	2	T43731	rapamycin/FKBP12 t
744	60.5	5.0	265	1	CTBOP	corticotropin / li	817	60.5	5.0	2436	2	AH2515	versican precursor
745	60.5	5.0	266	2	D71945	hypothetical prote	818	60.5	5.0	2549	2	A54837	F1003.12 protein -
746	60.5	5.0	268	2	A83651	hypothetical prote	819	60.5	5.0	3381	2	T42389	hypothetical prote
747	60.5	5.0	282	2	T37491	dnaj protein - fis	820	60.5	5.0	3600	2	D86161	conserved hypotet
748	60.5	5.0	308	2	T25250	hypothetical prote	821	60.5	5.0	4936	2	AD2665	hypothetical prote
749	60.5	5.0	315	2	AB1812	hypothetical prote	822	60.5	5.0	167	2	AB0304	conserved hypotet
750	60.5	5.0	317	2	G75041	ornithine carbamoy	823	60.5	5.0	174	2	AD2665	hypothetical prote
751	60.5	5.0	352	2	G84077	hypothetical prote	824	60.5	5.0	198	2	C97447	recombinase Sin -
752	60.5	5.0	367	2	T31750	hypothetical prote	825	60.5	5.0	202	2	S68609	hypothetical prote
753	60.5	5.0	370	2	G01639	peptidylprolyl iso	826	60.5	5.0	217	2	A98196	probable transposa
754	60.5	5.0	380	2	A45981	transmembrane prot	827	60.5	5.0	225	2	A86043	cytochrome c, tetr
755	60.5	5.0	386	2	S51436	probable membrane	828	60.5	5.0	233	2	B59037	signal peptidase I
756	60.5	5.0	398	2	B49211	phospholipase C, a	829	60.5	5.0	234	2	C75360	hypothetical prote
757	60.5	5.0	398	2	A30555	phospholipase C (E	830	60.5	5.0	242	2	T48519	hypothetical prote
758	60.5	5.0	406	2	T20330	hypothetical prote	831	60.5	5.0	247	2	C87628	probable membrane
759	60.5	5.0	409	2	B37753	NadR protein - Sal	832	60.5	5.0	255	2	AG0437	

833	60	5.0	274	2	G64854	ycfN protein - Esc	906	60	5.0	1354	2	T41262	mutS family DNA mi
834	60	5.0	281	1	ZBBE12	30.2K zinc-binding	907	60	5.0	1361	2	T41365	mutator 2 - fruit
835	60	5.0	306	2	S38251	follistatin-relate	908	60	5.0	1312	2	S68593	DNA-directed DNA p
836	60	5.0	308	2	G98150	diptide transpor	909	60	5.0	1438	2	S59792	probable membrane
837	60	5.0	315	2	T51683	myb-related trans	910	60	5.0	1641	2	I38614	helicase II - huma
838	60	5.0	328	2	A46521	52K phosphoprotein	911	60	5.0	1819	2	T32008	hypothetical prote
839	60	5.0	329	2	S55489	probable galactosy	912	60	5.0	1927	2	T25604	hypothetical prote
840	60	5.0	339	2	A91111	hypothetical prote	913	60	5.0	1997	1	S12050	protein-tyrosine-p
841	60	5.0	339	2	G85956	hypothetical prote	914	60	5.0	2183	2	T42764	coagulation factor
842	60	5.0	330	2	G90734	hypothetical prote	915	60	5.0	2264	1	GNVVTB	genome polyprotein
843	60	5.0	330	2	A55585	unknown protein en	916	60	5.0	2427	2	T16613	hypothetical prote
844	60	5.0	330	2	I57835	lymphocyte-specifi	917	60	5.0	3149	1	Q8BE8	BPLP1 protein - hu
845	60	5.0	347	2	T07140	glucan endo-1,3-be	918	60	5.0	3570	2	T45025	mucin MUC5B, trach
846	60	5.0	357	2	AC3645	flagellar p-ring p	919	60	5.0	3588	2	I40485	surfactin syntheta
847	60	5.0	362	2	S48270	hypothetical prote	920	60	5.0	4543	1	A53102	alpha-2-macroglobu
848	60	5.0	365	2	G72306	conserved hypotet	921	59.5	4.9	89	2	F90816	probable excisiona
849	60	5.0	371	2	T06382	Knox protein 1 - g	922	59.5	4.9	92	2	B85676	hypothetical prote
850	60	5.0	374	2	JC7091	centaurin alpha 1	923	59.5	4.9	94	2	D71284	hypothetical prote
851	60	5.0	399	2	JC4592	transcription fact	924	59.5	4.9	156	2	JQ1377	18K membrane prote
852	60	5.0	399	2	T09375	hypothetical prote	925	59.5	4.9	172	2	C72327	hypothetical prote
853	60	5.0	408	2	B84591	hypothetical prote	926	59.5	4.9	213	2	T03931	DNA binding protei
854	60	5.0	421	2	H81843	conserved hypotet	927	59.5	4.9	226	2	B85080	hypothetical prote
855	60	5.0	421	2	D81098	gcpB protein NMB13	928	59.5	4.9	262	2	D71557	hypothetical prote
856	60	5.0	422	2	A83317	carbamoyl-phosphat	929	59.5	4.9	290	2	A64693	fructose-1,6-bisph
857	60	5.0	422	2	G87188	phosphoribosylamin	930	59.5	4.9	293	2	S61983	regulatory protein
858	60	5.0	424	2	B95964	probable phosphono	931	59.5	4.9	307	2	D70741	hypothetical prote
859	60	5.0	427	2	A84667	probable MYB famil	932	59.5	4.9	318	1	YX8AT3	thymidylate synth
860	60	5.0	435	2	T03545	probable cobyrinic	933	59.5	4.9	318	2	T24509	hypothetical prote
861	60	5.0	437	2	A69128	aspartate-tRNA lig	934	59.5	4.9	320	2	T36823	probable integral
862	60	5.0	443	2	F90213	hypothetical prote	935	59.5	4.9	338	2	JE0196	hydroxysteroid sul
863	60	5.0	448	2	AF1942	hypothetical prote	936	59.5	4.9	342	2	E97601	hypothetical prote
864	60	5.0	454	1	A40858	GA-binding protein	937	59.5	4.9	342	2	E28223	agta [imported] -
865	60	5.0	454	2	D69177	hypothetical prote	938	59.5	4.9	353	2	T01978	hypothetical prote
866	60	5.0	459	2	T08594	probable sulfate a	939	59.5	4.9	355	2	B87473	acyl-CoA dehydrog
867	60	5.0	460	2	A24325	muscarinic acetyl	940	59.5	4.9	385	2	E95847	conserved hypotet
868	60	5.0	463	2	C86034	L-seryl-tRNAsecc se	941	59.5	4.9	393	2	S57050	cyclophilin-like p
869	60	5.0	463	2	D91187	L-seryl-tRNAsecc se	942	59.5	4.9	409	2	T42414	conserved hypotet
870	60	5.0	463	2	A65159	L-seryl-tRNAsecc se	943	59.5	4.9	413	2	S58865	probable membrane
871	60	5.0	483	2	A11908	hypothetical prote	944	59.5	4.9	414	2	H88481	L-rhamnose isomera
872	60	5.0	486	2	A64906	probable fructuron	945	59.5	4.9	418	2	H83843	probable two-compo
873	60	5.0	486	2	B86130	nannomate oxidore	946	59.5	4.9	422	2	E83083	sat1 protein - fis
874	60	5.0	486	2	B91289	D-mannomate oxidor	947	59.5	4.9	441	2	T43544	RNA polymerase sig
875	60	5.0	486	2	H85719	probable oxidoredu	948	59.5	4.9	447	2	AE1382	hypothetical prote
876	60	5.0	486	2	G90897	probable oxidoredu	949	59.5	4.9	452	2	B84483	hypothetical prote
877	60	5.0	492	2	H72473	probable phosphosu	950	59.5	4.9	461	2	E84474	hypothetical prote
878	60	5.0	495	2	AB0703	conserved hypotet	951	59.5	4.9	467	2	AF1317	ATP-dependent DNA
879	60	5.0	503	1	APECA	leucyl aminopeptid	952	59.5	4.9	476	2	S64953	hypothetical prote
880	60	5.0	503	2	E91283	aminopeptidase A/I	953	59.5	4.9	479	1	A42241	glycine hydroxymet
881	60	5.0	503	2	G86124	hypothetical prote	954	59.5	4.9	499	2	F69136	hypothetical prote
882	60	5.0	507	2	S74641	SHP substrate-1 pr	955	59.5	4.9	502	2	F84455	probable ribonucle
883	60	5.0	513	2	JC5289	hypothetical prote	956	59.5	4.9	516	2	D64207	glutamic acid spec
884	60	5.0	513	2	F70776	hypothetical prote	957	59.5	4.9	516	2	T40584	probable involveme
885	60	5.0	513	2	T05210	hypothetical prote	958	59.5	4.9	520	1	O4BQM	cholesterol monoox
886	60	5.0	514	2	B96585	hypothetical prote	959	59.5	4.9	524	2	JC7594	cytochrome P450 en
887	60	5.0	546	2	B85398	hypothetical prote	960	59.5	4.9	524	2	JC7598	cytochrome P450 en
888	60	5.0	563	2	S22837	probable membrane	961	59.5	4.9	525	2	S15207	methane monooxygen
889	60	5.0	568	2	H64879	ATP-dependent heli	962	59.5	4.9	530	2	T20360	hypothetical prote
890	60	5.0	643	2	H83873	methionine-tRNA li	963	59.5	4.9	530	2	T39942	Satip - fission ye
891	60	5.0	658	2	D69431	hypothetical prote	964	59.5	4.9	550	2	F87305	alkaline phosphata
892	60	5.0	670	2	F84540	cell cycle histidi	965	59.5	4.9	564	2	G75165	glucamyl-tRNA synt
893	60	5.0	691	2	B87383	RNA-directed RNA p	966	59.5	4.9	571	2	T20359	hypothetical prote
894	60	5.0	726	1	P21VBC	RNA-directed RNA p	967	59.5	4.9	580	2	AB0994	gamma-glutamyltran
895	60	5.0	726	1	P21VBW	RNA-directed RNA p	968	59.5	4.9	606	2	T51880	hypothetical prote
896	60	5.0	740	2	G95153	neuraminidase, pro	969	59.5	4.9	608	2	E90374	hypothetical prote
897	60	5.0	744	2	A82822	NADH-ubiquinone ox	970	59.5	4.9	619	2	S30780	hexose metabolism-
898	60	5.0	805	2	E97717	virB4 protein prec	971	59.5	4.9	630	2	S25796	hypothetical prote
899	60	5.0	805	2	T34212	hypothetical prote	972	59.5	4.9	638	2	S12136	somatotropin recep
900	60	5.0	835	2	F90260	hypothetical prote	973	59.5	4.9	654	2	AB3553	membrane protein r
901	60	5.0	886	2	A54442	3',5'-cyclic-nucle	974	59.5	4.9	662	1	A31349	arachidonate 15-li
902	60	5.0	925	2	T22388	hypothetical prote	975	59.5	4.9	679	2	T50445	conserved hypotet
903	60	5.0	1141	2	T20611	hypothetical prote	976	59.5	4.9	697	2	T26707	hypothetical prote
904	60	5.0	1193	2	A86193	hypothetical prote	977	59.5	4.9	715	2	S38051	DOAL protein - yea
905	60	5.0	1201	2	F81202	proline dehydrogen	978	59.5	4.9	716	2	G44490	retrovirus-related

979	59.5	4.9	769	2	F81415	DNA topoisomerase	1052	59	4.9	474	2	S75464	hypothetical prote
980	59.5	4.9	780	2	T35268	probable transcript	1053	59	4.9	475	2	F70972	probable amidase -
981	59.5	4.9	789	2	A30843	glutinin high mole	1054	59	4.9	476	1	JC6505	stromelysin 2 (EC
982	59.5	4.9	791	2	JN0690	glutinin, high-mol	1055	59	4.9	478	2	T34091	hypothetical prote
983	59.5	4.9	824	2	AD3098	periplasmic nitrat	1056	59	4.9	485	2	C75460	hypothetical prote
984	59.5	4.9	833	2	S62136	CWH41 protein - ye	1057	59	4.9	487	2	A11505	hypothetical cell
985	59.5	4.9	834	2	E98188	periplasmic nitrat	1058	59	4.9	493	2	AB0588	PTR2-family transp
986	59.5	4.9	851	2	S50670	BCK2 protein - yea	1059	59	4.9	495	2	T13025	hypothetical prote
987	59.5	4.9	876	2	T05943	probable lipoxigen	1060	59	4.9	506	2	AI0798	probable membrane
988	59.5	4.9	876	2	F97688	leucyl-tRNA synth	1061	59	4.9	514	2	C64154	hypothetical prote
989	59.5	4.9	876	2	AC2914	leucyl-tRNA synth	1062	59	4.9	540	2	A95264	probable ABC trans
990	59.5	4.9	900	2	A95340	cation transport p	1063	59	4.9	544	2	S58532	matk protein (trnk
991	59.5	4.9	902	2	B4652	hypothetical prote	1064	59	4.9	547	2	I39593	exea protein - Aer
992	59.5	4.9	973	2	A85055	probable leucyl tr	1065	59	4.9	549	1	B64557	hypothetical prote
993	59.5	4.9	1075	2	A80510	carbamoyl-phosphat	1066	59	4.9	552	1	S35703	probable ABC tran
994	59.5	4.9	1084	2	T33759	hypothetical prote	1067	59	4.9	552	1	A3401	hypothetical prote
995	59.5	4.9	1087	2	S88147	protein kinase - f	1068	59	4.9	555	2	H96762	matk protein (trnk
996	59.5	4.9	1139	2	B70954	hypothetical prote	1069	59	4.9	555	2	H96762	hypothetical prote
997	59.5	4.9	1171	2	A42916	metabotropic gluta	1070	59	4.9	558	2	E83583	probable acyl-CoA
998	59.5	4.9	1184	2	H86190	hypothetical prote	1071	59	4.9	603	2	T34901	probable gamma-glu
999	59.5	4.9	1262	2	T30524	protein phosphatas	1072	59	4.9	614	2	T39688	fibrin - fission
1000	59.5	4.9	1463	2	T30192	nuclear receptor c	1073	59	4.9	627	2	G97244	probable phosphogl
1001	59.5	4.9	1496	2	A00447	insecticidal toxin	1074	59	4.9	627	2	E70122	flagellar hook-ass
1002	59.5	4.9	1541	2	A24274	heterocyst glycoli	1075	59	4.9	639	1	B41328	1,4-alpha-glucan b
1003	59.5	4.9	1765	2	A31494	DNA-directed RNA p	1076	59	4.9	656	2	H82862	conjugal transfer
1004	59.5	4.9	1765	2	B31494	DNA-directed RNA p	1077	59	4.9	678	2	S28648	glutamate-cysteine
1005	59.5	4.9	1766	2	B31875	DNA-directed RNA p	1078	59	4.9	681	2	I78558	recombination repa
1006	59.5	4.9	1766	2	A31875	DNA-directed RNA p	1079	59	4.9	699	2	A83368	hypothetical Brach
1007	59.5	4.9	1791	2	T02345	hypothetical prote	1080	59	4.9	732	2	F84394	chitinase (EC 3.2.
1008	59.5	4.9	1876	2	C70749	probable ppsA prot	1081	59	4.9	745	2	T38299	probable beta-adap
1009	59.5	4.9	2222	1	A36028	DNA-directed prote	1082	59	4.9	767	2	A49546	DNA topoisomerase
1010	59.5	4.9	2531	2	T16743	hypothetical prote	1083	59	4.9	820	2	G82168	trimethylamine-N-o
1011	59.5	4.9	2617	2	A82136	peptide synthetase	1084	59	4.9	829	2	S72366	DNA topoisomerase
1012	59.5	4.9	3005	1	GNVSTV	genome polyprotein	1085	59	4.9	888	2	D84650	probable potassium
1013	59.5	4.9	3391	1	GNVTV16	genome polyprotein	1086	59	4.9	914	2	T00757	probable ubiquitin
1014	59	4.9	108	2	B43926	ORF 3' of ctsA - B	1087	59	4.9	966	1	PHPOAG	starch phosphoryla
1015	59	4.9	177	2	D83727	RNA polymerase ECF	1088	59	4.9	993	2	T09129	probable erythrocy
1016	59	4.9	181	1	TXSPM	thioredoxin m prec	1089	59	4.9	1011	2	A12046	ABC transporter At
1017	59	4.9	195	2	A96731	unknown protein F5	1090	59	4.9	1060	2	S63252	hypothetical prote
1018	59	4.9	202	2	T36368	hypothetical prote	1091	59	4.9	1074	2	T52654	Ca2+-transporting
1019	59	4.9	219	2	T09671	RPE15 protein - al	1092	59	4.9	1096	2	A96607	protein disease re
1020	59	4.9	227	2	A82318	riboflavin-specifi	1093	59	4.9	1103	2	T42022	probable chitin sy
1021	59	4.9	238	2	S38369	tetrahydromethanop	1094	59	4.9	1175	2	S39951	chitin synthase (E
1022	59	4.9	241	2	G70578	hypothetical prote	1095	59	4.9	1206	2	AG2140	hypothetical prote
1023	59	4.9	242	2	T40523	hypothetical prote	1096	59	4.9	1214	2	JC2069	zinc-finger protei
1024	59	4.9	244	2	AF2753	transcription regu	1097	59	4.9	1234	2	S72640	endo-1,4-beta-xyla
1025	59	4.9	252	2	D97534	probable transcript	1098	59	4.9	1288	2	T09908	hypothetical prote
1026	59	4.9	259	2	A27259	hypothetical rolB	1099	59	4.9	1290	2	S73653	DNA-directed RNA p
1027	59	4.9	268	2	T10304	inhibitor of apopt	1100	59	4.9	1345	2	S46817	hypothetical prote
1028	59	4.9	268	2	A53989	apoptosis-inhibiti	1101	59	4.9	1541	2	S46686	hypothetical prote
1029	59	4.9	277	1	RDHUCB	carboxyl reductase	1102	59	4.9	1664	2	T18262	S-layer protein -
1030	59	4.9	280	2	H95901	conserved hypotet	1103	59	4.9	1904	2	T13256	tail-host specific
1031	59	4.9	285	2	A86755	prophage p12 prote	1104	59	4.9	1992	1	S02771	myosin heavy chain
1032	59	4.9	294	2	AD1649	weakly phage relat	1105	59	4.9	2163	2	T15276	hypothetical prote
1033	59	4.9	296	2	AG3388	exodeoxyribonuclea	1106	59	4.9	3175	1	RRWVEV	genome polyprotein
1034	59	4.9	297	2	B83621	probable transcript	1107	59	4.9	9376	2	T14593	syngomycin synth
1035	59	4.9	304	2	A89882	hypothetical prote	1108	59	4.9	76	2	G87155	hypothetical prote
1036	59	4.9	305	2	G84568	probable xylogluca	1109	58.5	4.9	126	2	G83571	conserved hypotet
1037	59	4.9	330	2	A30533	lymphocyte-specifi	1110	58.5	4.9	154	2	J50710	heat shock protein
1038	59	4.9	334	2	AC0517	fructose repressor	1111	58.5	4.9	158	2	S16247	heat shock protein
1039	59	4.9	334	2	S15941	PEP-fructosephosph	1112	58.5	4.9	166	2	A81853	chaperone protein
1040	59	4.9	335	2	AD1686	peptidase homolog	1113	58.5	4.9	173	2	T29033	hypothetical prote
1041	59	4.9	348	2	C83571	probable binding p	1114	58.5	4.9	177	2	T47133	hypothetical prote
1042	59	4.9	362	2	C82070	conserved hypotet	1115	58.5	4.9	201	2	E70941	hypothetical prote
1043	59	4.9	373	1	S04039	alcohol dehydrogen	1116	58.5	4.9	202	2	E86476	protein F1504.41 [
1044	59	4.9	378	1	T03758	probable ferredoxi	1117	58.5	4.9	215	1	ASLJGG	conserved hypotet
1045	59	4.9	394	2	S77272	hypothetical prote	1118	58.5	4.9	216	2	AC0715	T-cell receptor ga
1046	59	4.9	397	2	I48717	proteinase inhibic	1119	58.5	4.9	234	2	B43546	afdB regulatory pr
1047	59	4.9	400	2	B97020	argininosuccinate	1120	58.5	4.9	243	2	A25037	hydrolase, alpha/b
1048	59	4.9	441	2	AG2337	hypothetical prote	1121	58.5	4.9	244	2	A87633	polysaccharide dea
1049	59	4.9	455	2	A11995	amino acid transpo	1122	58.5	4.9	257	2	C87550	conserved hypotet
1050	59	4.9	460	2	A31897	muscarinic acetyl	1123	58.5	4.9	258	2	AC0057	
1051	59	4.9	474	1	A40570	lipoprotein lipase	1124	58.5	4.9				

1125	58.5	4.9	258	2	T48687	hypotheical prote	1198	58.5	4.9	680	2	T25832	hypotheical prote
1126	58.5	4.9	269	2	G83865	hypotheical prote	1199	58.5	4.9	689	2	T35882	glycoprotein H - h
1127	58.5	4.9	273	2	S76948	probable creatinin	1200	58.5	4.9	690	2	T41950	hypotheical prote
1128	58.5	4.9	277	2	I39872	conserved hypotet	1201	58.5	4.9	706	2	S50616	hypotheical prote
1129	58.5	4.9	280	2	H87305	metallo-beta-lacta	1202	58.5	4.9	714	2	T16126	hypotheical prote
1130	58.5	4.9	283	2	H83860	pantothenate synth	1203	58.5	4.9	721	2	S29795	hypotheical prote
1131	58.5	4.9	292	2	A95163	hypotheical prote	1204	58.5	4.9	721	2	T09631	probable acylamino
1132	58.5	4.9	292	2	H98028	hypotheical prote	1205	58.5	4.9	728	2	B71009	hypotheical prote
1133	58.5	4.9	301	2	T75593	probable ABC trans	1206	58.5	4.9	746	2	T29584	outer capsid prote
1134	58.5	4.9	302	2	B36896	probable transamin	1207	58.5	4.9	776	2	A48480	hypotheical prote
1135	58.5	4.9	307	2	A96220	hypotheical prote	1208	58.5	4.9	802	2	T24448	hypotheical prote
1136	58.5	4.9	307	2	AH3066	conserved hypotet	1209	58.5	4.9	822	2	AE2404	DNA helicase [limp
1137	58.5	4.9	312	1	S73934	MG085 homolog G07	1210	58.5	4.9	848	2	S48273	probable transcrip
1138	58.5	4.9	314	1	S09575	osteopontin precu	1211	58.5	4.9	898	2	D95123	phosphoenolpyruvat
1139	58.5	4.9	317	2	G71119	probable ornithine	1212	58.5	4.9	931	2	D86222	protein F7G19.9 [i
1140	58.5	4.9	320	2	G96714	hypotheical prote	1213	58.5	4.9	983	2	AG2381	glycine cleavage s
1141	58.5	4.9	329	1	JGECA	L-arabinose-bindin	1214	58.5	4.9	994	2	T50309	hypotheical WD-re
1142	58.5	4.9	329	2	A98905	L-arabinose-bindin	1215	58.5	4.9	993	2	JQ0488	afar protein - Str
1143	58.5	4.9	329	2	F85853	probable regulator	1216	58.5	4.9	1007	2	G96606	disease resistance
1144	58.5	4.9	337	2	T34964	hypotheical prote	1217	58.5	4.9	1040	1	T46931	alpha-mannosidase
1145	58.5	4.9	340	2	T18650	homeotic protein H	1218	58.5	4.9	1054	1	A69375	NADPH-ferrihemopro
1146	58.5	4.9	367	2	G71076	probable hydrogena	1219	58.5	4.9	1058	2	B95148	carbamoyl-phosphat
1147	58.5	4.9	371	2	C87446	queuine tRNA ribos	1220	58.5	4.9	1058	2	H98015	carbamoyl-phosphat
1148	58.5	4.9	381	2	G83518	probable acyl-CoA	1221	58.5	4.9	1091	2	B71322	isoleucine-tRNA li
1149	58.5	4.9	388	2	T31322	carbamoyl phosphat	1222	58.5	4.9	1092	2	S42798	fibronectin-bindin
1150	58.5	4.9	388	2	AC0138	tolA colicin impo	1223	58.5	4.9	1097	2	T31504	hypotheical prote
1151	58.5	4.9	394	2	S76353	probable aspartate	1224	58.5	4.9	1165	2	A48667	peroxisomal assemb
1152	58.5	4.9	402	2	S75082	pantothenate metab	1225	58.5	4.9	1168	1	MXAXIC	myosin heavy chain
1153	58.5	4.9	403	2	H69362	succinyl-diaminopi	1226	58.5	4.9	1266	2	T27024	hypotheical prote
1154	58.5	4.9	406	2	T50894	hydroxyneuroporen	1227	58.5	4.9	1338	2	T40993	protein kinase cek
1155	58.5	4.9	409	2	D75629	probable transposa	1228	58.5	4.9	1402	2	H86560	protein export [im
1156	58.5	4.9	410	2	A59279	beta-arrestin 2 -	1229	58.5	4.9	1402	2	E72062	hypotheical prote
1157	58.5	4.9	414	2	H90815	probable kinase [i	1230	58.5	4.9	1405	2	T27969	hypotheical prote
1158	58.5	4.9	414	2	D85675	probable kinase yc	1231	58.5	4.9	1421	2	T49500	hypotheical prote
1159	58.5	4.9	421	2	C64856	probable permesase	1232	58.5	4.9	1477	2	T00957	myosin heavy chain
1160	58.5	4.9	421	2	C82253	folylpolyglutamate	1233	58.5	4.9	1626	2	A75613	hypotheical prote
1161	58.5	4.9	422	2	A10145	probable substrate	1234	58.5	4.9	1704	2	T43141	vitellogenin 1 - m
1162	58.5	4.9	425	2	A84849	probable RING zinc	1235	58.5	4.9	1768	2	T27023	hypotheical prote
1163	58.5	4.9	439	2	A35744	clusterin precuro	1236	58.5	4.9	2109	2	I38414	transcription fact
1164	58.5	4.9	443	2	T05132	hypotheical prote	1237	58.5	4.9	2150	1	S27802	zinc finger protei
1165	58.5	4.9	446	2	G70634	probable lipp prot	1238	58.5	4.9	2150	2	T19450	hypotheical prote
1166	58.5	4.9	450	2	A11671	signal recognition	1239	58.5	4.9	2342	2	T18200	fatty-acid synthas
1167	58.5	4.9	464	1	S37616	transcription fact	1240	58.5	4.9	2588	2	AI2136	peptide synthase
1168	58.5	4.9	465	2	AE0931	two-component syst	1241	58.5	4.9	3512	2	T17121	CFR protein - midg
1169	58.5	4.9	471	2	S42631	microsome-associat	1242	58	4.8	115	2	B97764	hypotheical prote
1170	58.5	4.9	472	2	G01872	selenium-binding p	1243	58	4.8	137	2	AC2864	lactoylglutathione
1171	58.5	4.9	474	2	B64434	anthranilate synth	1244	58	4.8	148	2	AC0254	conserved hypotet
1172	58.5	4.9	477	1	KCHUS1	stromelysin 1 (EC	1245	58	4.8	153	2	F97641	probable lactoylgl
1173	58.5	4.9	486	2	T18903	hypotheical prote	1246	58	4.8	158	2	H83350	hypotheical prote
1174	58.5	4.9	489	2	T41446	conserved hypotet	1247	58	4.8	166	2	S22631	petp protein - Rho
1175	58.5	4.9	495	2	AH0517	UDP-N-acetyluramo	1248	58	4.8	169	2	D65126	probable general s
1176	58.5	4.9	505	2	H95390	probable reverse t	1249	58	4.8	171	2	T51674	myb-related trans
1177	58.5	4.9	506	2	B87102	conserved membrane	1250	58	4.8	175	2	C70326	hypotheical prote
1178	58.5	4.9	506	2	F83545	hypotheical prote	1251	58	4.8	177	2	T09495	thioredoxin m - ra
1179	58.5	4.9	507	1	A32966	cytochrome P450 4A	1252	58	4.8	190	2	B95210	hypotheical prote
1180	58.5	4.9	511	1	JQ1935	endo-1,4-beta-xyla	1253	58	4.8	190	2	E98074	hypotheical prote
1181	58.5	4.9	540	2	B87350	hypotheical prote	1254	58	4.8	191	1	RGBY36	cell division cont
1182	58.5	4.9	548	2	T04058	protoporphyrinogen	1255	58	4.8	210	2	AC2468	transcription anti
1183	58.5	4.9	562	2	S75651	hypotheical prote	1256	58	4.8	213	2	AH2253	hypotheical prote
1184	58.5	4.9	570	2	F71049	glutamine-tRNA lig	1257	58	4.8	218	2	H07770	probable regulator
1185	58.5	4.9	575	2	C34106	protein kinase (EC	1258	58	4.8	220	2	G85872	probable lipoprote
1186	58.5	4.9	579	2	T15135	hypotheical prote	1259	58	4.8	224	2	B91111	hypotheical prote
1187	58.5	4.9	609	2	S28283	hypotheical prote	1260	58	4.8	224	2	B85956	hypotheical prote
1188	58.5	4.9	613	2	AB1964	cell division prot	1261	58	4.8	238	2	D69021	tetrahydromethanop
1189	58.5	4.9	614	2	D34106	protein kinase (EC	1262	58	4.8	246	2	S46604	2-deoxyglucose-6-p
1190	58.5	4.9	619	2	E84800	hypotheical prote	1263	58	4.8	250	2	AF2881	lipase esterase [i
1191	58.5	4.9	619	2	G84489	probable TNP2-like	1264	58	4.8	250	2	F97657	lipase esterase (A
1192	58.5	4.9	626	2	D90069	sulfite reductase	1265	58	4.8	250	2	T05996	hypotheical prote
1193	58.5	4.9	626	2	F85295	hypotheical prote	1266	58	4.8	258	2	T13263	hypotheical prote
1194	58.5	4.9	627	2	T05789	hypotheical prote	1267	58	4.8	259	2	AE2435	hypotheical prote
1195	58.5	4.9	657	2	S73946	excinuclease ABC c	1268	58	4.8	264	2	S74721	tryptophan synthas
1196	58.5	4.9	672	2	B82015	probable integral	1269	58	4.8	266	2	AI2283	hypotheical prote
1197	58.5	4.9	678	2	B83154	conserved hypotet	1270	58	4.8	275	2	A82578	glycerol uptake fa

1271	58	4.8	296	2	F72745	hypothetical prote	1344	58	4.8	663	1	A38283	arachidonate 12-11
1272	58	4.8	300	2	B85021	hypothetical prote	1345	58	4.8	664	2	S44756	probable protein d
1273	58	4.8	302	2	T36030	probable fructokin	1346	58	4.8	679	2	T00636	hypothetical prote
1274	58	4.8	303	2	A00980	glycine-tRNA ligas	1347	58	4.8	686	2	A38235	microtubule-associ
1275	58	4.8	306	2	A24119	ornithine carbamoy	1348	58	4.8	695	2	T40451	n-terminal acetyle
1276	58	4.8	311	2	T02009	hypothetical prote	1349	58	4.8	698	1	TVFVLV	protein-tyrosine k
1277	58	4.8	312	2	C94511	hypothetical prote	1350	58	4.8	698	2	C96001	probable glycosyl
1278	58	4.8	322	2	A57516	DNA supercoiling f	1351	58	4.8	704	2	S46000	probable membrane
1279	58	4.8	330	2	G95187	conserved domain p	1352	58	4.8	724	2	C83706	antibiotic mersac
1280	58	4.8	333	2	A32284	proline racemase (1353	58	4.8	757	2	AF1755	DNA topoisomerase
1281	58	4.8	337	2	A52228	dolichol-phosphate	1354	58	4.8	767	2	JU0144	ferrous iron trans
1282	58	4.8	337	2	S55932	NCA3 protein precu	1355	58	4.8	771	2	AI0016	outer layer protei
1283	58	4.8	339	2	B83496	hypothetical prote	1356	58	4.8	776	1	A45395	exoribonuclease RN
1284	58	4.8	339	2	AC2153	hypothetical prote	1357	58	4.8	793	2	AI1380	hypothetical prote
1285	58	4.8	342	2	S42885	beta-1,3-glucanase	1358	58	4.8	796	2	T23238	hypothetical prote
1286	58	4.8	344	2	E75629	probable integrase	1359	58	4.8	798	2	T00131	xylan 1,4-beta-xyl
1287	58	4.8	358	2	C72626	hypothetical prote	1360	58	4.8	800	2	T23247	hypothetical prote
1288	58	4.8	367	2	H96764	protein RING zinc	1361	58	4.8	808	1	EEWTHW	glutinin, high mol
1289	58	4.8	370	2	A46579	estrogen receptor-	1362	58	4.8	867	1	JQ1525	nitrate reductase
1290	58	4.8	375	2	T02215	ferredoxin-NADP re	1363	58	4.8	880	2	F85381	potassium channel-
1291	58	4.8	376	1	B65183	probable hydro-lya	1364	58	4.8	898	2	JH0440	RAD54 protein - ye
1292	58	4.8	376	2	D91219	probable regulator	1365	58	4.8	916	2	T05360	probable potassium
1293	58	4.8	376	2	F86065	probable regulator	1366	58	4.8	923	2	A53054	lipoxxygenase (EC 1
1294	58	4.8	377	2	C96111	beta-lactamase, pe	1367	58	4.8	948	2	E82206	DnaK-related prote
1295	58	4.8	377	2	C91270	beta-lactamase [im	1368	58	4.8	952	2	T44754	probable glycine d
1296	58	4.8	377	2	C86873	transcription regu	1369	58	4.8	964	2	T41547	hypothetical prote
1297	58	4.8	388	2	A82903	conserved hypotet	1370	58	4.8	973	2	T50449	DNA repair and rec
1298	58	4.8	392	2	A49208	nitrite reductase	1371	58	4.8	1039	2	I38401	ATP-driven ion pum
1299	58	4.8	398	2	J00366	phospholipase C (E	1372	58	4.8	1043	2	D84900	hypothetical prote
1300	58	4.8	399	2	A53856	aryl-acylamidase (1373	58	4.8	1051	2	A40021	integrin alpha-3 c
1301	58	4.8	406	2	J70357	Rep protein - Clos	1374	58	4.8	1065	2	A43421	SEC8 protein - yea
1302	58	4.8	407	2	G84309	hypothetical prote	1375	58	4.8	1073	2	I51055	recombination acti
1303	58	4.8	407	2	T33427	hypothetical prote	1376	58	4.8	1095	2	T01916	hypothetical prote
1304	58	4.8	420	2	T08691	hypothetical prote	1377	58	4.8	1097	2	A56138	transcription fact
1305	58	4.8	425	2	T27241	hypothetical prote	1378	58	4.8	1132	2	C75259	probable iron-sulf
1306	58	4.8	435	2	T15737	hypothetical prote	1379	58	4.8	1174	2	T08196	hypothetical prote
1307	58	4.8	437	2	H90265	heterodisulfite re	1380	58	4.8	1213	2	E69255	mannosyltransferas
1308	58	4.8	438	2	S61589	TVA protein - yea	1381	58	4.8	1240	2	S21086	anion exchange pro
1309	58	4.8	440	2	C94553	probable protein k	1382	58	4.8	1299	2	D87226	conserved hypotet
1310	58	4.8	440	2	T17220	hypothetical prote	1383	58	4.8	1322	2	T39371	transcription regu
1311	58	4.8	443	2	C94553	hypothetical prote	1384	58	4.8	1770	2	S69948	TyB protein - yea
1312	58	4.8	469	2	B95958	probable glucurona	1385	58	4.8	1771	2	S53592	TyB protein - yea
1313	58	4.8	478	2	S69974	TyA protein - yea	1386	58	4.8	1810	2	S69973	TyB protein - yea
1314	58	4.8	484	2	T17756	probable chitinase	1387	58	4.8	2958	2	S64921	probable membrane
1315	58	4.8	497	2	JB0275	voltage-gated pota	1388	58	4.8	3534	2	T42567	tegument protein 2
1316	58	4.8	499	2	AC2128	ferrichrome-iron r	1389	58	4.8	4861	2	S71752	giant protein p619
1317	58	4.8	504	2	T38226	probable serine-th	1390	57.5	4.8	72	2	AB3232	entry-exclusion pr
1318	58	4.8	516	2	A86148	hypothetical prote	1391	57.5	4.8	114	2	S72940	hypothetical prote
1319	58	4.8	517	2	JC7623	protein disulfide-	1392	57.5	4.8	132	2	E82403	hypothetical prote
1320	58	4.8	519	2	S74242	6-phosphofructo-2-	1393	57.5	4.8	144	2	T50076	probable 50S ribos
1321	58	4.8	527	2	S39549	thioglucosidase (E	1394	57.5	4.8	151	2	S21600	heat shock protein
1322	58	4.8	529	2	T50609	hypothetical prote	1395	57.5	4.8	154	2	S12629	heat shock cognate
1323	58	4.8	530	2	B84130	two-component resp	1396	57.5	4.8	158	2	B64864	ycgN protein - Esc
1324	58	4.8	541	2	B95220	dextran glucosidas	1397	57.5	4.8	158	2	D90838	hypothetical prote
1325	58	4.8	541	2	H98083	dehydranase (EC 3.2	1398	57.5	4.8	158	2	D85696	hypothetical prote
1326	58	4.8	550	2	AB0166	probable prismane	1399	57.5	4.8	162	2	B87655	conserved hypotet
1327	58	4.8	555	2	H84476	hemagglutinin-neur	1400	57.5	4.8	176	2	B75015	dtdd-4-keto-i-rham
1328	58	4.8	565	1	HNNZSV	hypothetical prote	1401	57.5	4.8	202	2	H85666	phosphatase/kinase
1329	58	4.8	576	2	T17842	lipoprotein a limp	1402	57.5	4.8	206	2	H84865	probable glutathio
1330	58	4.8	578	2	B90578	gamma-glutamyltran	1403	57.5	4.8	209	2	S30541	prolactin precurs
1331	58	4.8	586	2	A41125	gp13 protein - Myc	1404	57.5	4.8	216	2	T38897	hypothetical prote
1332	58	4.8	595	2	B72801	hypothetical prote	1405	57.5	4.8	228	2	C70164	rRNA methylase (ya
1333	58	4.8	604	2	T20875	hypothetical prote	1406	57.5	4.8	229	2	D83250	cytidylate kinase
1334	58	4.8	612	1	W1WLE	Ei protein - human	1407	57.5	4.8	237	2	C75035	arginase related p
1335	58	4.8	631	2	G64874	probable membrane	1408	57.5	4.8	241	2	E75064	hypothetical prote
1336	58	4.8	640	2	G72339	threonine-tRNA lig	1409	57.5	4.8	243	2	T38519	hypothetical prote
1337	58	4.8	645	2	T39614	kinase-binding pro	1410	57.5	4.8	246	2	B86260	protein T12C24.18
1338	58	4.8	645	2	A75533	conserved hypotet	1411	57.5	4.8	251	2	S23889	hypothetical prote
1339	58	4.8	646	2	T48644	negative regulator	1412	57.5	4.8	252	2	AH2105	hypothetical prote
1340	58	4.8	647	1	E5ECPC	2',3'-cyclic-nucle	1413	57.5	4.8	253	2	A32187	triose-phosphate i
1341	58	4.8	647	1	G86118	2',3'-cyclic-nucle	1414	57.5	4.8	255	2	B87595	transcription regu
1342	58	4.8	647	1	G91277	2',3'-cyclic-nucle	1415	57.5	4.8	264	1	E70027	probable 3-oxoacyl
1343	58	4.8	649	2	H90163	DNA-directed RNA p	1416	57.5	4.8	265	2	AG0814	cob(I)alamin adeno

Db 142 SGDNRGKFKVESFRKKYHLGAPVACTCFQAE-WDDS 176

RESULT 2

T31721
hypothetical protein F40A3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31721
R;Geisels, C.; Bradshaw, H.; Keppler, D.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid F40A3.
A;Reference number: Z21074
A;Accession: T31721
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-221 <GEI>
A;Cross-references: UNIPROT:O16264; EMBL:AF016423; PIDN:AAB5322.1; GSPDB:GN00023; CESP:
A;Experimental source: strain Bristol N2; clone F40A3
C;Genetics:
A;Gene: CESP:F40A3.3
A;Map position: 5
A;Introns: 32/2; 70/3
C;Superfamily: Caenorhabditis elegans hypothetical protein Y69E1A.5

Query Match 19.5%; Score 234.5; DB 2; Length 221;
Best Local Similarity 33.1%; Pred. No. 1.1e-15;
Matches 58; Conservative 16; Mismatches 60; Indels 41; Gaps 6;
QY 59 KVPDP--CNNYRQKITSMWPIVKFPGAVD-----GATYIL 92
Db 46 EVIPDLVASPPSKVWS-----VKFSGVEANLGNVLTPTQVKDTPSVKWDAPFGALYTL 100
QY 93 VMVDPDAPSRAEPRQRFWRHLVTDIKGADLKKGKIQGELSAYQAPSPPAHSGFHRHYQF 152
Db 101 IKTFDAPSRKEPYRERHHLVWNIPENDIAK-----GDTLSEYIGAGPPPKTGLHRYVY 156
QY 153 FVYLQEGKVIS-----LLPKENKTRGSKMDRFLNRFHLGEPPEASTQFMTQNTQD 202
Db 157 LIYKQSGRIEDAEHGRLTNTSGDKRGCKAAADFVAKHKLGAIPVFGNLFQAE-YDD 210

RESULT 3

PC4214
phosphatidylethanolamine binding protein Ovd3 - nematode (Onchocerca volvulus) (fragment)
C;Species: Onchocerca volvulus
C;Date: 17-Dec-1996 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: PC4214
R;Erttmann, K.D.; Gallin, M.Y.
Gene 174, 203-207, 1996
A;Title: Onchocerca volvulus: Identification of cDNAs encoding a putative phosphatidy-
A;Reference number: PC4214; MUID:97045813; PMID:8890735
A;Accession: PC4214
A;Molecule type: mRNA
A;Residues: 1-134 <ERT>
A;Cross-references: UNIPROT:P54188; EMBL:X87989; NID:g1143530; PID:g1143531
C;Genetics:
A;Introns: 34/3; 52/2; 81/1; 129/3
C;Superfamily: Caenorhabditis elegans hypothetical protein Y69E1A.5

Query Match 18.5%; Score 223; DB 2; Length 134;
Best Local Similarity 36.3%; Pred. No. 8.6e-15;
Matches 53; Conservative 18; Mismatches 59; Indels 16; Gaps 5;
QY 55 NIGCKVVP--DCNNYRQKITSMWPIVKFPGAVDGYTLVMVDPDAPSRAEPRQRFWRHW 113
Db 2 NLGNELTPTQVKQPTKV-SW-----DAEPGALYTLVMTDPAKRNKPNVFRFHHW 52
QY 114 LVTDIKGADLKKGKIQGELSAYQAPSPPAHSGFHRHYQFVYLQEGKVISLPLPKENKTRG 173
Db 53 LIINISQNVSSGTV-----LSDYIGSGQPKGTGLHRYVFLVYKQPGSITD--TQHGGRNP 106
QY 174 SKWMDRFLNRFHLGEPPEASTQFMTQNTQ 199

Db 107 NFKVMDFANKHHLGNFVAGNFFQAKH 132

RESULT 4

PC4216
phosphatidylethanolamine binding protein Ovd1 - nematode (Onchocerca volvulus) (fragment)
C;Species: Onchocerca volvulus
C;Date: 17-Dec-1996 #sequence_revision 21-Jan-1997 #text_change 20-Jun-2000
C;Accession: PC4216
R;Erttmann, K.D.; Gallin, M.Y.
Gene 174, 203-207, 1996
A;Title: Onchocerca volvulus: Identification of cDNAs encoding a putative phosphatidy-
A;Reference number: PC4214; MUID:97045813; PMID:8890735
A;Accession: PC4216
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-152 <ERT>
A;Cross-references: EMBL:X87991
C;Comment: This protein is involved in odorant binding and is located in the chemosensory
C;Superfamily: Caenorhabditis elegans hypothetical protein Y69E1A.5

Query Match 18.4%; Score 222; DB 2; Length 152;
Best Local Similarity 36.3%; Pred. No. 1.3e-14;
Matches 53; Conservative 18; Mismatches 59; Indels 16; Gaps 5;
QY 55 NIGCKVVP--DCNNYRQKITSMWPIVKFPGAVDGYTLVMVDPDAPSRAEPRQRFWRHW 113
Db 20 NLGNELTPTQVKQPTKV-SW-----DAEPGALYTLVMTDPAKRNKPNVFRFHHW 70
QY 114 LVTDIKGADLKKGKIQGELSAYQAPSPPAHSGFHRHYQFVYLQEGKVISLPLPKENKTRG 173
Db 71 LIINISQNVSSGTV-----LSDYIGSGRKGTLHRYVFLVYKQPGSITD--TQHGGRNP 124
QY 174 SKWMDRFLNRFHLGEPPEASTQFMTQNTQ 199
Db 125 NFKVMDFANKHHLGNFVAGNFFQAKH 150

RESULT 5

S00056
basic cytosolic protein, 21k - bovine
N;Alternate names: phosphatidylethanolamine-binding protein
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: S00056; S51191
R;Schoentgen, F.; Saccoccio, F.; Jolles, J.; Bernier, I.; Jolles, P.
Eur. J. Biochem. 166, 333-338, 1987
A;Title: Complete amino acid sequence of a basic 21-kDa protein from bovine brain cytosol
A;Reference number: S00056; MUID:87275914; PMID:3609012
A;Accession: S00056
A;Molecule type: protein
A;Residues: 1-186 <SCH>
A;Cross-references: UNIPROT:P13696
A;Experimental source: brain
R;Bucquoy, S.; Jolles, P.; Schoentgen, F.
Eur. J. Biochem. 225, 1203-1210, 1994
A;Title: Relationships between molecular interactions (nucleotides, lipids and proteins)
A;Reference number: S51191; MUID:95045550; PMID:7957211
A;Contents: annotation
C;Superfamily: Caenorhabditis elegans hypothetical protein Y69E1A.5
C;Keywords: brain; cytosol; lipid binding; nucleotide binding; phospholipid
F;112-125/Region: nucleotide binding
F;168-182/Region: lipid binding

Query Match 18.1%; Score 218.5; DB 2; Length 186;
Best Local Similarity 33.3%; Pred. No. 3.6e-14;
Matches 53; Conservative 24; Mismatches 65; Indels 17; Gaps 4;
QY 46 LEVFY--PELGNIGKVVDPDCNNYRQKITSMWPIVKFPGAVDGYTLVMVDPDAPRA 103
Db 24 LQVKYGGAEVDLGNLTVTQVKRNPSTIW-----DGLDPGKLYTLVLTDPDAPSRK 76

[illegible]

Science 286, 1962-1965, 1999
A;Title: Activation tagging of the floral inducer FT.
A;Reference number: Z26027
A;Accession: T52303
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-175 <KAR>
A;Cross-references: EMBL:AFI52907; PIDN:AAF03937.1
A;Experimental source: cultivar Columbia
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke,
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16991
A;Accession: T10579
A;Molecule type: DNA
A;Residues: 1-175 <BEV>
A;Cross-references: EMBL:AL080253; GSPDB:GN00062; ATSP:F9F13.20
A;Experimental source: cultivar Columbia; BAC clone F9F13
C;Genetics:
A;Gene: TSP; ATSP:F9F13.20
A;Map position: 4
A;Introns: 67/3; 88/2; 102/1
C;Function:
A;Description: promotes flowering [validated, MUID:20050958]; involved in induction of t t
A;Note: is positively regulated by transcription factor CONSTANS
C;Superfamily: Caenorhabditis elegans hypothetical protein Y69E1A.5

Query Match 15.1%; Score 182; DB 2; Length 175;
Best Local Similarity 36.2%; Pred. No. 1.4e-10;
Matches 46; Conservative 15; Mismatches 50; Indels 16; Gaps 4;

Qy 76 EPVKKFGAVDGATYILVMVDPDAPSRAEPRQRFWRHVLVTDIKGADLKGKIQGOELSA 135
Db 51 KPIVEIGDDFRNFYTLVMVDPDVPSPHQREYVHLVLTIDIPAT---TGNAFGNEVVC 107
Qy 136 YQAPSPPAHSGFHYQFYVLOEGKVISLIPKENKTRGSKWMD---RFLNRFLGGEPEA 191
Db 108 YESFRPP--SGIHRVLVLFQRLGRQTYAP-----GWRQFNTREFAEIYNLGLPEVA 158
Qy 192 STQFMQTQ 198
Db 159 ASYFNCQ 165

RESULT 12
A57391
TcSL-2 protein precursor - Toxocara canis
C;Species: Toxocara canis
C;Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 09-Jul-2004
C;Accession: A57391
R;Gems, D.; Ferguson, C.J.; Robertson, B.D.; Nieves, R.; Page, A.P.; Blaxter, M.L.; Maize
J. Biol. Chem. 270, 18517-18522, 1995
A;Title: An abundant, trans-spliced mRNA from Toxocara canis infective larvae encodes a ;
A;Reference number: A57391; MUID:95355481; PMID:7629180
A;Accession: A57391
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-262 <GEM>
A;Cross-references: UNIPROT:P54190; GB:U29761; NID:g881974; PIDN:AAC46843.1; PID:g881975
A;Note: the mature mRNA is trans-spliced and contain the leader sequence SL1
C;Keywords: duplication
F;1-20/Domain: signal sequence #status predicted <SIG>

Query Match 14.1%; Score 169.5; DB 2; Length 262;
Best Local Similarity 27.2%; Pred. No. 4.2e-09;
Matches 56; Conservative 27; Mismatches 86; Indels 37; Gaps 5;

Qy 25 DENSPCAHEALLDDETLF-----CGLEVFYPELGNIGCKVVP----- 62
Db 61 DEANNCASINLCONPFFELVRDRCKTCGLCAGCGFISGIVPLVTSAPSRVSTF 120
Qy 63 -----DCNNYRKITSWMEPIVKFPGAVGATYILVMVDPDAPSRAEPRQRFWRHVLVT 116
Db 121 ANNQVQNCGNLTATQAVANQFTWTE-AQPNDRYTLIMVDPDFPSAANGQGOQLHWVI 179

[illegible]

RESULT 13

T52447
PT protein [validated] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52447
R;Kobayashi, Y.; Kaya, H.; Goto, K.; Iwabuchi, M.; Araki, T.
Science 286, 1960-2, 1999
A;Title: A pair of related genes with antagonistic roles in mediating flowering signals
A;Reference number: Z25350; MUID:20050958; PMID:10583960
A;Accession: T52447
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-175 <KOB>
A;Cross-references: UNIPROT:Q9SXZ2; EMBL:AB027504; PIDN:BAA77838.1
A;Experimental source: cultivar Landsberg erecta
C;Genetics:
A;Gene: FT
A;Map position: 1
C;Function:
A;Description: promotes flowering [validated, MUID:20050958]
A;Pathway: is positively regulated by transcription factor CONSTANS
C;Superfamily: Caenorhabditis elegans hypothetical protein Y69E1A.5

	Query Match	13.6%	Score 164;	DB 2;	Length 175;
	Best Local Similarity	36.3%;	Pred. No. 9e-09;		
	Matches	41;	Conservative	13;	Mismatches 43; Indels 16; Gaps 4;
QY	90	YILVMVDPDPSRAEPRQRWRHVLVTDIIKGADLKKGIQOELSAVQAQSPPPAHSGFHR	149		
DB	65	YTLVMVDPDVPSPNPHRLBYHLVTDIPAT---TGTTFGNEIVCYENPSPTA--GIHR	119		
QY	150	YQFVVVLQEGKVLSLLPKENKTRGSKWMD-----RFLRPHLGEPEASTQPMQTQ	198		
DB	120	WVPIRLQGRQTVYAP-----GWRQNFRTREFAEIIYNLGLPVAAVFNVCQ	165		

RESULT 14

T07877
self-pruning protein - tomato
N/Alternate names: centroradialis protein ortholog
C/Species: Lycopersicon esculentum (tomato)
C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
R/Accession: T07877
C/Rnucli: L.; Carmel-Goren, L.; Hareven, D.; Gutfinger, T.; Alvarez, J.; Ganai, M.; Zandi
Development 125, 1979-1989, 1998
A/Rtitle: The SELF-PRUNING gene of tomato regulates vegetative to reproductive switching
A/Reference number: Z16190; MUID:98237698; PMID:9570763
A/Accession: T07877
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-175 <PNU>
A/Cross-references: UNIPROT:O82088; EMBL:U84140; NID:g3319211; PIDN:AAC26161.1; PID:g3319211
C/Genetics:
A/Gene: sp
C/Superfamily: Caenorhabditis elegans hypothetical protein Y69E1A.5

Query Match	12.3%	Score 148.5;	DB 2;	Length 175;
Best Local Similarity	31.3%;	Pred. No. 3.1e-07;		
Matches 42;	Conservative 24;	Mismatches 55;	Indels 13;	Gaps 6;

45	FPSSVTS--	XPRVEVHGDDLRSF	FTLIMIDPDVPGSDPYLREHLHWIVTDIPGTTDCSF	102
Qy	126	GKTCQQLSAYQAPSP	PAHSGFHRQYFVYLQCK-VISLLPKENKTRGSKWQDFLNRF	184
Db	103	GR----	EVGYEMPRP--NIGIHRFVLLFKOKKQTISSAP---VSRDQFSSRKPFSEEN	153
Qy	185	HLGPEASTQFM	TQ 198	
Db	154	ELGSPVA	AVFENCQ 167	

RESULT 15

S68507
centroradialis protein - garden snapdragon
N;Alternate names: GRP-binding protein homolog
C;Species: Antirrhinum majus (garden snapdragon)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C;Accession: S68507; S78126
R;Bradley, D.; Carpenter, R.; Copsey, L.; Vincent, C.; Rothstein, S.; Coen, E.
Nature 379, 791-797, 1996
A;Title: Control of inflorescence architecture in Antirrhinum.
A;Reference number: S68507; MUID:96172853; PMID:5897601
A;Accession: S68507
A;Molecule type: mRNA
A;Residues: 1-181 <BRA>
A;Cross-references: UNIPROT:Q41261; EMBL:S81193; NID:G1336806; PID:G1336807
A;Accession: S78126
A;Molecule type: DNA
A;Residues: 1-181 <BRB>
C;Genetics: cn
A;Gene: cnb
F;Superfamily: Caenorhabditis elegans hypothetical protein Y69E1A.5
F;116-132/Region: nucleotide binding #status predicted

Query Match	12.3%	Score 148;	DB 2;	Length 181;
Best Local Similarity	29.1%	Pred. No. 3.7e-07;		
Matches	44;	Conservative	25;	Mismatches 62; Indels 20; Gaps 5;
Qy	60	VVPDCNN-----VRQKITSNMEPIVKPFGAVDGYTILWVMDPAPSRAPERQR	108	
Db	31	VIYNSNNSIKHVNNGHELFPSSAVTS--TPRVEVHGDMRSFFTLIIMTDPDVGSPDPVLR	88	
Qy	109	FWRHRLWTDIKG-ADLKKGKIQOQLSAYQAPSPAHSGFHRQYFFVYLOEGKVISLTPK	167	
Db	89	EHLHWIIVTDIPGTTSDSSFGK----EVVSVMYMRP--NIGTHRFVFLLPKQKRCQAMLSP	142	
Qy	168	ENKTRSGWKMDRFLNRFHLGCEPEASTQFWTQ	198	
Db	143	PVVCRDGFNTRKFTQENELGLPVAAVFFNCQ	173	

Search completed: January 30, 2005, 17:09:10
Job time : 70 secs

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OM protein - protein search, using sw model

Run on: January 30, 2005, 17:06:38 ; Search time 77 Seconds
(without alignments)
1046.332 Million cell up

Title: US-10-035-958-61

Perfect score:

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Scoring table: BLOSUM62

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Searched: 1608061 seqs. 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

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Post-processing: Minimum Match 0%

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Listing first 1500 summaries

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272	91	7.6	17	10	US-10-369-493-930	Sequence 930, App	345	75.5	6.3	1504	17	US-10-101-235A-4	Sequence 4, Appli
273	91	7.6	17	10	US-09-895-298-222	Sequence 222, App	346	75	6.2	164	14	US-10-425-115-351847	Sequence 351847, A
274	91	7.6	179	9	US-10-885-039-222	Sequence 222, App	347	75	6.2	417	16	US-10-029-386-34205	Sequence 34205, A
275	89.5	7.4	176	9	US-10-156-761-14011	Sequence 14011, A	348	75	6.2	569	14	US-10-437-963-153712	Sequence 153712, A
276	89.5	7.4	176	10	US-09-791-171-50	Sequence 50, Appl	349	75	6.2	980	16	US-10-369-493-19251	Sequence 19251, A
277	89.5	7.4	176	10	US-09-943-443-50	Sequence 50, Appl	350	75	6.2	1041	13	US-10-451-467A-32	Sequence 1406, Ap
278	89.5	7.4	176	16	US-09-804-980-50	Sequence 50, Appl	351	74.5	6.2	193	16	US-10-369-493-1935	Sequence 1935, Ap
279	89.5	7.4	196	16	US-10-620-246-50	Sequence 50, Appl	352	74.5	6.2	206	15	US-10-767-701-55269	Sequence 55269, A
280	88.5	7.4	174	9	US-10-408-765A-2170	Sequence 2170, Ap	353	74.5	6.2	236	14	US-10-424-599-137857	Sequence 137857, A
281	88.5	7.4	209	15	US-09-902-331-8	Sequence 8, Appli	354	74.5	6.2	265	14	US-10-424-599-137857	Sequence 79, Appl
282	88	7.3	87	17	US-10-425-114-41291	Sequence 41291, A	355	74.5	6.2	265	14	US-10-235-173-79	Sequence 79, Appl
283	88	7.3	167	9	US-10-425-115-211755	Sequence 211755, A	356	74.5	6.2	311	14	US-10-237-386-62	Sequence 62, Appl
284	88	7.3	167	16	US-09-902-331-4	Sequence 4, Appli	357	74.5	6.2	339	14	US-10-369-493-14114	Sequence 14114, A
285	88	7.3	267	11	US-10-437-963-153847	Sequence 153847, A	358	74.5	6.2	455	14	US-10-369-493-17559	Sequence 17559, A
286	88	7.3	297	11	US-09-985-153-122	Sequence 122, App	359	74.5	6.2	531	14	US-10-369-493-5340	Sequence 5340, Ap
287	87	7.2	89	16	US-09-985-153-66	Sequence 66, Appl	360	74.5	6.2	686	14	US-10-369-493-17970	Sequence 17970, A
288	87	7.2	165	9	US-10-655-799-27	Sequence 27, Appl	361	74	6.1	233	17	US-10-011-548-4	Sequence 4, Appli
289	85.5	7.1	273	15	US-09-902-331-12	Sequence 12, Appl	362	74	6.1	319	15	US-10-835-641-25	Sequence 25, Appl
290	85.5	7.1	490	10	US-10-108-260A-2625	Sequence 2625, Ap	363	74	6.1	504	17	US-10-282-122A-60415	Sequence 60415, A
291	85.5	7.1	490	17	US-09-992-238-7	Sequence 7, Appli	364	74	6.1	504	15	US-10-739-930-5971	Sequence 5971, Ap
292	85	7.1	165	9	US-10-712-615-7	Sequence 7, Appli	365	74	6.1	548	16	US-10-072-012-863	Sequence 863, App
293	83.5	6.9	274	16	US-09-902-331-14	Sequence 14, Appl	366	74	6.1	548	16	US-10-451-467A-80	Sequence 480, App
294	83.5	6.9	275	9	US-10-755-889-32	Sequence 32, Appl	367	74	6.1	1061	15	US-10-451-467A-674	Sequence 674, App
295	83	6.9	232	16	US-10-437-963-113293	Sequence 113293, A	368	74	6.1	2038	15	US-10-425-114-53914	Sequence 53914, A
296	83	6.9	595	14	US-10-170-385-319	Sequence 319, App	369	74	6.1	2092	14	US-10-433-794-18	Sequence 18, Appl
297	82	6.8	198	16	US-10-437-963-114393	Sequence 114393, A	370	74	6.1	2092	15	US-10-377-035-18	Sequence 18, Appl
298	82	6.8	357	15	US-10-424-599-242626	Sequence 242626, A	371	74	6.1	2429	16	US-10-042-865-79	Sequence 79, Appl
299	81.5	6.8	177	9	US-09-738-626-5179	Sequence 5179, Ap	372	74	6.1	2429	15	US-10-408-765A-1967	Sequence 1967, Ap
300	80.5	6.7	76	17	US-10-425-115-272042	Sequence 272042, A	373	74	6.1	2429	14	US-10-288-798-8	Sequence 8, Appli
301	79.5	6.6	62	16	US-10-425-115-272042	Sequence 272042, A	374	73.5	6.1	213	17	US-10-377-035-17	Sequence 17, Appl
302	79.5	6.6	170	15	US-10-767-701-50212	Sequence 50212, A	375	73.5	6.1	287	14	US-10-363-892-8	Sequence 8, Appli
303	79.5	6.6	358	15	US-10-424-599-197858	Sequence 197858, A	376	73.5	6.1	419	15	US-10-425-115-354530	Sequence 354530, A
304	79.5	6.6	358	17	US-10-425-114-69560	Sequence 69560, A	377	73.5	6.1	429	15	US-10-369-493-20884	Sequence 20884, A
305	79.5	6.6	595	15	US-10-425-115-353049	Sequence 353049, A	378	73.5	6.1	503	9	US-10-424-599-176279	Sequence 176279, A
					US-10-080-334-247	Sequence 247, App						US-10-072-012-445	Sequence 445, App
												US-09-944-807-4	Sequence 44, Appli

379	73.5	6.1	503	13	US-10-087-993-37	Sequence 37, Appl	452	70.5	5.9	732	16	US-10-322-281-769	Sequence 769, App
380	73.5	6.1	503	14	US-10-290-198-6	Sequence 6, Appl	453	70.5	5.9	830	14	US-10-369-493-22142	Sequence 22142, A
381	73.5	6.1	503	15	US-10-072-012-442	Sequence 44, App	454	70.5	5.9	1067	17	US-10-425-115-298658	Sequence 298658, A
382	73.5	6.1	503	16	US-10-874-015-4	Sequence 44, Appl	455	70.5	5.9	1213	17	US-10-425-115-212446	Sequence 212446, A
383	73.5	6.1	504	15	US-10-072-012-441	Sequence 44, App	456	70.5	5.9	1293	16	US-10-437-963-166420	Sequence 166420, A
384	73.5	6.1	504	16	US-10-408-765A-2185	Sequence 2185, App	457	70.5	5.9	1641	16	US-10-437-963-166420	Sequence 166420, A
385	73.5	6.1	504	16	US-10-437-963-104780	Sequence 104780, App	458	70.5	5.9	1737	16	US-10-437-963-195758	Sequence 195758, A
386	73.5	6.1	561	16	US-10-087-192-1572	Sequence 1572, App	459	70.5	5.8	122	17	US-10-425-115-195895	Sequence 195895, A
387	73.5	6.1	1102	13	US-10-087-192-1572	Sequence 1572, App	460	70.5	5.8	131	16	US-10-437-963-198021	Sequence 198021, A
388	73.5	6.1	1103	13	US-10-334-143-4	Sequence 4, Appl	461	70.5	5.8	166	16	US-10-767-701-59626	Sequence 59626, A
389	73.5	6.1	1388	16	US-10-408-765A-1139	Sequence 1139, App	462	70.5	5.8	309	9	US-09-864-761-33397	Sequence 33397, A
390	73	6.1	419	15	US-10-369-493-2854	Sequence 2854, App	463	70.5	5.8	316	9	US-09-815-242-10795	Sequence 10795, A
391	73	6.1	458	11	US-09-950-822-2	Sequence 2, Appl	464	70.5	5.8	354	9	US-09-731-872-416	Sequence 416, App
392	73	6.1	458	11	US-09-950-822-10	Sequence 10, Appl	465	70.5	5.8	354	15	US-09-876-997-701	Sequence 10, Appl
393	73	6.1	508	14	US-10-128-714-3500	Sequence 3500, App	466	70.5	5.8	354	15	US-10-415-187-10	Sequence 10, Appl
394	73	6.1	508	14	US-10-128-714-4028	Sequence 4028, App	467	70.5	5.8	359	15	US-10-282-122A-49088	Sequence 49088, A
395	73	6.1	747	17	US-10-408-765A-538	Sequence 538, App	468	70.5	5.8	402	15	US-10-072-012-443	Sequence 443, App
396	73	6.1	747	17	US-10-723-860-1294	Sequence 1294, App	469	70.5	5.8	438	9	US-09-950-902-2	Sequence 2, Appl
397	72.5	6.0	85	15	US-10-424-599-243757	Sequence 243757, App	470	70.5	5.8	485	14	US-10-183-687-421	Sequence 421, App
398	72.5	6.0	158	17	US-10-425-115-304627	Sequence 304627, App	471	70.5	5.8	485	14	US-10-183-687-426	Sequence 426, App
399	72.5	6.0	158	17	US-10-425-115-304633	Sequence 304633, App	472	70.5	5.8	503	15	US-10-072-012-120	Sequence 120, App
400	72.5	6.0	158	17	US-10-425-115-304634	Sequence 304634, App	473	70.5	5.8	784	15	US-10-282-122A-66570	Sequence 66570, A
401	72.5	6.0	159	17	US-10-425-115-291948	Sequence 291948, App	474	70.5	5.8	806	14	US-10-363-493-3678	Sequence 3678, App
402	72.5	6.0	214	15	US-10-282-122A-61966	Sequence 61966, A	475	70.5	5.8	813	17	US-10-425-115-200019	Sequence 200019, A
403	72.5	6.0	321	15	US-10-424-599-243757	Sequence 243757, App	476	70.5	5.8	1417	15	US-10-282-122A-51059	Sequence 51059, A
404	72.5	6.0	327	13	US-10-042-417-58	Sequence 58, Appl	477	70.5	5.8	1839	14	US-10-032-585-7605	Sequence 7605, App
405	72.5	6.0	327	16	US-10-679-246-12	Sequence 12, Appl	478	70.5	5.8	2137	15	US-10-042-865-81	Sequence 81, Appl
406	72.5	6.0	379	15	US-10-264-049-2807	Sequence 2807, App	479	70.5	5.8	2432	15	US-10-112-944-359	Sequence 359, App
407	72.5	6.0	708	15	US-10-264-237-1835	Sequence 1835, App	480	70.5	5.8	2503	16	US-10-322-281-723	Sequence 723, App
408	72.5	6.0	731	16	US-10-408-765A-2869	Sequence 2869, App	481	70.5	5.8	2545	15	US-10-042-865-12	Sequence 12, Appl
409	72.5	6.0	857	17	US-10-425-115-297634	Sequence 297634, App	482	69.5	5.8	263	17	US-10-822-613-32	Sequence 32, Appl
410	72.5	6.0	951	17	US-10-425-115-297634	Sequence 297634, App	483	69.5	5.8	277	14	US-10-238-075-682	Sequence 682, App
411	72.5	6.0	1054	17	US-10-425-115-297634	Sequence 297634, App	484	69.5	5.8	307	17	US-10-437-963-203506	Sequence 203506, A
412	72.5	6.0	1102	10	US-09-974-573-1	Sequence 1, Appl	485	69.5	5.8	329	15	US-10-425-115-212326	Sequence 212326, A
413	72.5	6.0	1193	13	US-10-071-900-4	Sequence 4, Appl	486	69.5	5.8	423	14	US-10-424-599-210519	Sequence 210519, A
414	72.5	6.0	1211	14	US-10-242-943-14	Sequence 14, Appl	487	69.5	5.8	466	15	US-10-032-585-7180	Sequence 7180, App
415	72.5	6.0	1211	14	US-10-242-943-14	Sequence 14, Appl	488	69.5	5.8	478	15	US-10-425-114-46206	Sequence 46206, A
416	72.5	6.0	2210	13	US-10-035-895-2	Sequence 2, Appl	489	69.5	5.8	484	15	US-10-425-114-40095	Sequence 40095, A
417	72.5	6.0	275	15	US-10-282-122A-55720	Sequence 55720, A	490	69.5	5.8	588	15	US-10-282-122A-57342	Sequence 57342, A
418	72.5	6.0	299	9	US-09-808-602-63	Sequence 63, Appl	491	69.5	5.8	588	15	US-10-424-599-276806	Sequence 276806, A
419	72.5	6.0	299	14	US-10-029-386-32938	Sequence 32938, A	492	69.5	5.8	775	14	US-10-227-110-70	Sequence 70, Appl
420	72.5	6.0	379	14	US-10-425-114-59560	Sequence 59560, A	493	69.5	5.8	775	14	US-10-208-508-70	Sequence 70, Appl
421	72.5	6.0	448	15	US-10-437-963-187075	Sequence 187075, App	494	69.5	5.8	817	14	US-10-369-493-10372	Sequence 10372, A
422	72.5	6.0	643	16	US-10-369-493-18865	Sequence 18865, A	495	69.5	5.8	856	16	US-10-437-963-169892	Sequence 169892, A
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424	71.5	5.9	158	17	US-10-425-115-321986	Sequence 321986, App	497	69.5	5.8	1250	16	US-10-437-963-194363	Sequence 194363, A
425	71.5	5.9	168	17	US-10-425-115-321986	Sequence 321986, App	498	69.5	5.8	1250	16	US-10-437-963-194363	Sequence 194363, A
426	71.5	5.9	194	17	US-10-425-115-304640	Sequence 304640, App	499	69.5	5.8	2029	15	US-10-087-684-38	Sequence 38, Appl
427	71.5	5.9	203	17	US-10-425-115-304624	Sequence 304624, App	500	69.5	5.8	2029	15	US-10-218-779-38	Sequence 39, Appl
428	71.5	5.9	210	15	US-10-425-114-65296	Sequence 65296, A	501	69.5	5.8	2037	15	US-10-087-684-39	Sequence 39, Appl
429	71.5	5.9	258	15	US-10-424-599-217157	Sequence 217157, App	502	69.5	5.8	2037	15	US-10-218-779-39	Sequence 151, App
430	71.5	5.9	551	16	US-10-437-963-132976	Sequence 132976, App	503	69.5	5.8	2041	16	US-10-408-765A-1151	Sequence 1151, App
431	71.5	5.9	712	14	US-10-369-493-2081	Sequence 2081, App	504	69.5	5.8	2270	16	US-10-408-765A-800	Sequence 800, App
432	71.5	5.9	725	15	US-10-282-122A-65371	Sequence 65371, A	505	69.5	5.8	2300	16	US-10-437-963-195865	Sequence 195865, A
433	71.5	5.9	725	15	US-10-282-122A-65746	Sequence 65746, A	506	69.5	5.8	2300	16	US-10-437-963-195865	Sequence 195865, A
434	71.5	5.9	747	15	US-10-022-366A-2	Sequence 2, Appl	507	69.5	5.7	212	9	US-09-425-021-21	Sequence 21, Appl
435	71.5	5.9	774	15	US-10-282-122A-43232	Sequence 43232, App	508	69.5	5.7	214	15	US-10-411-037-55	Sequence 55, Appl
436	71.5	5.9	1005	14	US-10-369-493-19100	Sequence 19100, A	509	69.5	5.7	214	15	US-10-411-026-55	Sequence 55, Appl
437	71.5	5.9	2030	16	US-10-437-963-195849	Sequence 195849, App	510	69.5	5.7	214	15	US-10-410-962-55	Sequence 55, Appl
438	71	5.9	316	15	US-10-282-122A-57056	Sequence 57056, A	511	69.5	5.7	214	16	US-10-410-930-55	Sequence 55, Appl
439	71	5.9	659	15	US-10-282-122A-58500	Sequence 58500, A	512	69.5	5.7	214	16	US-10-410-997-55	Sequence 55, Appl
440	71	5.9	721	15	US-10-424-599-210271	Sequence 210271, App	513	69.5	5.7	214	16	US-10-411-012-55	Sequence 55, Appl
441	71	5.9	860	16	US-10-437-963-197193	Sequence 197193, App	514	69.5	5.7	214	16	US-10-287-994-55	Sequence 55, Appl
442	71	5.9	1498	17	US-10-723-860-2399	Sequence 2399, App	515	69.5	5.7	214	16	US-10-410-913-55	Sequence 55, Appl
443	71	5.9	1944	16	US-10-408-765A-545	Sequence 545, App	516	69.5	5.7	233	16	US-10-660-128-9	Sequence 9, Appl
444	70.5	5.9	71	14	US-10-356-631-15	Sequence 15, Appl	517	69.5	5.7	234	14	US-10-045-674-587	Sequence 587, App
445	70.5	5.9	184	14	US-10-197-666A-28	Sequence 28, Appl	518	69.5	5.7	245	9	US-09-797-941A-6	Sequence 6, Appl
446	70.5	5.9	184	14	US-10-024-298A-81	Sequence 81, Appl	519	69.5	5.7	261	15	US-10-424-599-263009	Sequence 263009, A
447	70.5	5.9	184	14	US-10-042-211A-81	Sequence 81, Appl	520	69.5	5.7	329	14	US-10-146-772-248	Sequence 248, App
448	70.5	5.9	184	15	US-10-617-217A-81	Sequence 81, Appl	521	69.5	5.7	329	15	US-10-241-742-248	Sequence 248, App
449	70.5	5.9	184	17	US-10-024-298A-81	Sequence 81, Appl	522	69.5	5.7	329	15	US-10-440-523-248	Sequence 248, App
450	70.5	5.9	550	17	US-10-425-115-359860	Sequence 359860, App	523	69.5	5.7	329	15	US-10-440-523-248	Sequence 248, App
451	70.5	5.9	606	16	US-10-437-963-180130	Sequence 180130, App	524	69.5	5.7	329	15	US-10-461-925-248	Sequence 248, App

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527	69	5-7	347	15	US-10-424-599-263008	Sequence 263008,	600	68	5-6	603	17	US-10-788-792-188	Sequence 188, App
528	69	5-7	433	17	US-10-425-115-268697	Sequence 268697,	601	68	5-6	629	16	US-10-437-963-174374	Sequence 174374,
529	69	5-7	515	16	US-10-437-963-204377	Sequence 204377,	602	68	5-6	634	16	US-10-437-963-190016	Sequence 190016,
530	69	5-7	544	16	US-10-437-963-171334	Sequence 171334,	603	68	5-6	848	16	US-10-437-963-118012	Sequence 118012,
531	69	5-7	623	15	US-10-424-599-186206	Sequence 186206,	604	68	5-6	1056	16	US-10-437-963-164735	Sequence 164735,
532	69	5-7	672	14	US-10-094-749-2085	Sequence 2085, Ap	605	68	5-6	1202	16	US-10-437-963-103812	Sequence 103812,
533	69	5-7	752	16	US-10-322-281-772	Sequence 772, App	606	68	5-6	1681	15	US-10-037-417-20	Sequence 20, Appl
534	69	5-7	773	14	US-10-270-875-35	Sequence 35, Appl	607	68	5-6	1697	15	US-10-037-417-68	Sequence 68, Appl
535	69	5-7	773	14	US-10-270-878-35	Sequence 35, Appl	608	68	5-6	1723	15	US-10-037-417-18	Sequence 18, Appl
536	69	5-7	773	14	US-10-270-786-35	Sequence 35, Appl	609	68	5-6	1841	17	US-10-425-115-360657	Sequence 360657,
537	69	5-7	773	14	US-10-270-710-35	Sequence 35, Appl	610	68	5-6	1867	15	US-10-466-759-4	Sequence 4, Appli
538	69	5-7	773	14	US-10-270-859-35	Sequence 35, Appl	611	68	5-6	1929	15	US-10-210-281-58	Sequence 58, Appl
539	69	5-7	773	14	US-10-270-846-35	Sequence 35, Appl	612	68	5-6	1962	15	US-10-084-846A-6	Sequence 6, Appli
540	69	5-7	1045	14	US-10-104-047-2830	Sequence 2830, Ap	613	67.5	5-6	128	17	US-10-425-115-216794	Sequence 216794,
541	69	5-7	1064	17	US-10-763-692-4	Sequence 4, Appli	614	67.5	5-6	158	16	US-10-767-701-45529	Sequence 45529, A
542	69	5-7	1223	17	US-10-425-115-321581	Sequence 321581,	615	67.5	5-6	158	17	US-10-425-115-199017	Sequence 199017,
543	69	5-7	1287	16	US-10-437-963-135124	Sequence 135124,	616	67.5	5-6	164	14	US-10-097-065-664	Sequence 664, App
544	69	5-7	1339	14	US-10-082-830-282	Sequence 282, App	617	67.5	5-6	164	14	US-10-372-876-664	Sequence 664, App
545	68.5	5-7	157	17	US-10-425-115-298875	Sequence 298875,	618	67.5	5-6	165	14	US-10-097-065-256	Sequence 256, App
546	68.5	5-7	169	14	US-10-156-761-14995	Sequence 14995, A	619	67.5	5-6	165	14	US-10-372-876-237	Sequence 237, App
547	68.5	5-7	170	17	US-10-425-115-357743	Sequence 357743,	620	67.5	5-6	277	15	US-10-282-122A-63420	Sequence 63420, A
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549	68.5	5-7	194	16	US-10-767-701-57892	Sequence 57892, A	622	67.5	5-6	284	15	US-10-425-114-49266	Sequence 49266, A
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733	67	5.6	412	14	US-10-245-473-14	Sequence 14, Appl	806	67	5.6	412	14	US-10-243-505-14	Sequence 14, Appl
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860	67	5.6	412	14	US-10-013-927A-157	Sequence 157, App	933	66.5	5.5	88	17	US-10-425-115-196297	Sequence 196297, A
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965	66	5.5	680	14	US-10-128-714-8183	Sequence 8183, App	1038	65.5	5.4	442	17	US-10-885-039-139	Sequence 139, App
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971	66	5.5	738	14	US-10-107-857-30	Sequence 30, App	1044	65.5	5.4	539	14	US-10-295-027-1299	Sequence 1299, App
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973	66	5.5	746	9	US-09-738-973-185	Sequence 185, App	1046	65.5	5.4	539	17	US-10-783-528-82	Sequence 82, App
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988	66	5.5	908	14	US-10-309-422-10	Sequence 10, App	1061	65.5	5.4	715	13	US-09-759-1308-73	Sequence 73, App
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1004	66	5.5	1091	14	US-10-309-422-12	Sequence 12, App	1077	65.5	5.4	1379	16	US-10-437-963-113781	Sequence 113781, App
1005	66	5.5	1092	14	US-10-309-422-24	Sequence 24, App	1078	65.5	5.4	1578	16	US-10-437-963-183595	Sequence 183595, App
1006	66	5.5	1126	14	US-10-309-422-16	Sequence 16, App	1079	65.5	5.4	1737	16	US-10-437-963-194264	Sequence 194264, App
1007	66	5.5	1127	14	US-10-309-422-28	Sequence 28, App	1080	65.5	5.4	1864	9	US-09-832-292-27	Sequence 27, App
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1016	65.5	5.4	234	14	US-10-333-574-19	Sequence 19, App	1089	65	5.4	180	15	US-10-223-650-44	Sequence 44, App
1017	65.5	5.4	234	14	US-10-043-487-226	Sequence 226, App	1090	65	5.4	185	17	US-10-739-930-6865	Sequence 6865, App
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1019	65.5	5.4	279	9	US-09-738-626-3632	Sequence 3632, App	1092	65	5.4	185	15	US-10-437-963-177085	Sequence 177085, App
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										459	11	US-09-950-822-11	Sequence 11, App

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1121	65	5.4	629	15	US-10-344-741-23	Sequence 23, Appl	1194	64.5	5.4	128	15	US-10-051-874-154	Sequence 154, App
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1303	64	5.3	237	16	US-10-762-967-6	Sequence 6, Appl	1376	64	5.3	1751	14	US-10-435-766-103	Sequence 17, Appl
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; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 61
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-342-61

Query Match 100.0%; Score 1204; DB 13; Length 223;
Best Local Similarity 100.0%; Pred. No. 5.3e-119;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGMTMLVTAALLGLMMVVTGDEDNPCAEHALDDETLFCQGLEVFYFPELGNIGCKV 60
DB 1 MGMTMLVTAALLGLMMVVTGDEDNPCAEHALDDETLFCQGLEVFYFPELGNIGCKV 60

QY 61 VPDNNYRQKITSWMEPIVKFPGAVDGAIVLVNVPDAPSRAPRQRFWRHMLVTDIKG 120
DB 61 VPDNNYRQKITSWMEPIVKFPGAVDGAIVLVNVPDAPSRAPRQRFWRHMLVTDIKG 120

QY 121 ADLKGKIQOELSAQAQSPPAHSGFHRVQFFVYLQEGKVISLLPKENKTRGSWKMDRF 180
DB 121 ADLKGKIQOELSAQAQSPPAHSGFHRVQFFVYLQEGKVISLLPKENKTRGSWKMDRF 180

QY 181 LNRFLHGEPEASTQFMTQNYQDSPTTLQAPRGRASEPKHKTRQ 223
DB 181 LNRFLHGEPEASTQFMTQNYQDSPTTLQAPRGRASEPKHKTRQ 223

RESULT 3
US-10-036-041-61
; Sequence 61, Application US/10036041
; Publication No. US20020192751A1
; GENERAL INFORMATION:
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030RICH
; CURRENT APPLICATION NUMBER: US/10/036,041
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300

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; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
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; PRIOR APPLICATION NUMBER: 60/115552
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22
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; PRIOR FILING DATE: 1999-03-23
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; PRIOR APPLICATION NUMBER: 60/125826
; PRIOR FILING DATE: 1999-03-24
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; PRIOR APPLICATION NUMBER: 60/127706
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; PRIOR FILING DATE: 1999-10-29
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; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
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; PRIOR FILING DATE: 2000-08-22
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; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
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; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02

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; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
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; PRIOR FILING DATE: 2001-02-28
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; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 61
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-041-61

Query Match 100.0%; Score 1204; DB 13; Length 223;
Best Local Similarity 100.0%; Pred. No. 5.3e-119;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWTMLVTAALLGLMMVVTGDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
DB 1 MGWTMLVTAALLGLMMVVTGDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60

QY 61 VPDNNYRQKITSMWEPVVKFPGAVDGYLVVMDPDAPSPRAEPQRQRFWRHVLVTDIKG 120
DB 61 VPDNNYRQKITSMWEPVVKFPGAVDGYLVVMDPDAPSPRAEPQRQRFWRHVLVTDIKG 120

QY 121 ADLKGKIQGQELSAQAPSPPAHSGFHYQFFVYLOEGKVISLLPKENKTRGSWKMDRF 180
DB 121 ADLKGKIQGQELSAQAPSPPAHSGFHYQFFVYLOEGKVISLLPKENKTRGSWKMDRF 180

QY 181 LNRPHLGEPEASTQFMTQYQDSPTLQAPGRASEPKHKTRQR 223
DB 181 LNRPHLGEPEASTQFMTQYQDSPTLQAPGRASEPKHKTRQR 223

RESULT 4
US-10-035-855-61
; Sequence 61, Application US/10035855
; Publication No. US20030008348A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3030P1C4
CURRENT APPLICATION NUMBER: US/10/035.855
PRIOR FILING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113430
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PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/114140
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115552
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/116843
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/125774
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/125778
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/125826
PRIOR FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: 60/127035
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/127706
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PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 09/311832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380142
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PRIOR FILING DATE: 2001-06-05

PRIOR APPLICATION NUMBER: 09/869599
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/908,827
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US99/10733
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PRIOR FILING DATE: 1999-12-02
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PRIOR APPLICATION NUMBER: PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
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PRIOR APPLICATION NUMBER: PCT/US00/34956
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PRIOR FILING DATE: 2001-02-28
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PRIOR FILING DATE: 2001-06-01
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PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 61
LENGTH: 223
TYPE: PRT
ORGANISM: Homo Sapien
US-10-035-855-61

Query Match 100.0%; Score 1204; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 5.3e-119;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGWTLRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFPELGNICKV	60
Db	1	MGWTLRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFPELGNICKV	60
Qy	61	VPDCNNYRQKITSWMEPIVKFPGAVDGTATYLVVMDPDAPSRAEPRQRFWRHMLVTDIKG	120
Db	61	VPDCNNYRQKITSWMEPIVKFPGAVDGTATYLVVMDPDAPSRAEPRQRFWRHMLVTDIKG	120
Qy	121	ADLKGKIQOQELSAQAPSPPAHSGFHRYPFYVYQEGKVISLLPKENKTRGSKWMDRF	180
Db	121	ADLKGKIQOQELSAQAPSPPAHSGFHRYPFYVYQEGKVISLLPKENKTRGSKWMDRF	180
Qy	181	LNRFHLEGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQ	223
Db	181	LNRFHLEGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQ	223

RESULT 5
US-10-227-884-232
Sequence 232, Application US/10227884
Publication No. US20030027988A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC79
CURRENT FILING DATE: 2002-08-26
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-10-28
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
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PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
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PRIOR FILING DATE: 1999-08-31
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PRIOR APPLICATION NUMBER: 60/166361
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PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 1204; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 5.3e-119;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGMTMLVTAALLGLMMVVTGDEDENSPCAHEALLDDETLFCOGLVEFVPELGNIGCKV 60
DB 1 MGMTMLVTAALLGLMMVVTGDEDENSPCAHEALLDDETLFCOGLVEFVPELGNIGCKV 60
QY 61 VPCNNYRQKITSMEPIVKFPGAVDGTATILVMVDPDAPSPRAEPRQRFWRHMLVTDIKG 120
DB 61 VPCNNYRQKITSMEPIVKFPGAVDGTATILVMVDPDAPSPRAEPRQRFWRHMLVTDIKG 120
QY 121 ADLKKGIQOQLSAYQAPSPHSGFHRVQFFVYLOEGKVISLLPKENTRGSWKMDRF 180
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QY 181 LNRPHLGEPEASTQFMTQNTQDSPTLQAPGRASEPKHKTRQR 223
DB 181 LNRPHLGEPEASTQFMTQNTQDSPTLQAPGRASEPKHKTRQR 223

RESULT 6
US-10-036-214-61
; Sequence 61, Application US/10036214
; Publication No. US20030032061A1

GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3030RIC11
; CURRENT APPLICATION NUMBER: US/10/036, 214
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
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;; PRIOR APPLICATION NUMBER: PCT/US01/21066
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: PCT/US01/21735
;; PRIOR FILING DATE: 2001-07-09
;; NUMBER OF SEQ ID NOS: 80
;; SEQ ID NO 61
;; LENGTH: 223
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-036-214-61

Query Match 100.0%; Score 1204; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 5.3e-119;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGWTRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFPELGNICKV 60
Db 1 MGWTRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFPELGNICKV 60

Qy 61 VPDCNNYRQKITSNWEPVVKPFGAVDGTATILVMVDPDAPSRAPRQRFWRHMLVTDIKG 120
Db 61 VPDCNNYRQKITSNWEPVVKPFGAVDGTATILVMVDPDAPSRAPRQRFWRHMLVTDIKG 120

Qy 121 ADLKKGIQOGLSAYQAPSPAHSGFHRVQFFVYLOEGKVISLTPKENKTRGSKWMDRF 180
Db 121 ADLKKGIQOGLSAYQAPSPAHSGFHRVQFFVYLOEGKVISLTPKENKTRGSKWMDRF 180

Qy 181 LNRPHLGEPEASTQFMTQNYQDSPTLOAPRGRASEPKHKTRQ 223

Db 181 LNRPHLGEPEASTQFMTQNYQDSPTLOAPRGRASEPKHKTRQ 223

RESULT 7
US-10-035-719-61
; Sequence 61, Application US/10035719
; Publication No. US20030036114A1
; GENERAL INFORMATION:
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030RIC2
; CURRENT APPLICATION NUMBER: US/10/035,719
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
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; PRIOR APPLICATION NUMBER: 60/115552
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; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 61
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-035-719-61

Query Match      100.0%; Score 1204; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 5.3e-119;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      121  ADLKKGIQOELSAYQAPSPPAHSGFHRQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
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Qy      181  LNRPHLGEPEASTQFMTQNYQDSPTTLOAPGRASEPKHKTRQR 223
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Db      181  LNRPHLGEPEASTQFMTQNYQDSPTTLOAPGRASEPKHKTRQR 223
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RESULT 8
US-10-230-163-232
; Sequence 232, Application US/10230163
; Publication No. US20030036635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deenoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: F3530F1C96
; CURRENT APPLICATION NUMBER: US/10/230,163
; CURRENT FILING DATE: 2002-08-28
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; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
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51	PRIOR FILING DATE: 1999-07-28
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66	PRIOR APPLICATION NUMBER: 60/169495
67	PRIOR FILING DATE: 1999-12-07
68	PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 1204; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 5.3e-119;
Matches 223; Conservative 0; Mismatches 0; Indels 0;

QY 1 MGMTLRVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCOGLVFFYPGLGNIGCKV 60
Db 1 MGMTLRVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCOGLVFFYPGLGNIGCKV 60
QY 61 VPCNNYRQKITSWMEPIVKFPGAVDGCATYILVMVDPDAPSPRAEPQRFRWHLVTDIKG 120
Db 61 VPCNNYRQKITSWMEPIVKFPGAVDGCATYILVMVDPDAPSPRAEPQRFRWHLVTDIKG 120
QY 121 ADLKKGKIQOELSAVOAPSPPAHSGFHRVQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
Db 121 ADLKKGKIQOELSAVOAPSPPAHSGFHRVQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
QY 181 LNRFLHGEPEASTQFMONTQNTQDSPTLQAPRGRASEPKHKTRQ 223
Db 181 LNRFLHGEPEASTQFMONTQNTQDSPTLQAPRGRASEPKHKTRQ 223

RESULT 9

US-10-036-160-61
; Sequence 61, Application US/10036160
; Publication No. US2003004842A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C3
; CURRENT APPLICATION NUMBER: US/10/036,160
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
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; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
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; PRIOR APPLICATION NUMBER: 60/116843
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; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/129122
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/130359
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131272
; PRIOR FILING DATE: 1999-04-27

; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/132371
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; PRIOR APPLICATION NUMBER: 60/135750
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/138166
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/146970
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/311832
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; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747259
; PRIOR FILING DATE: 2000-12-20
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; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
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; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
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; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 61
; LENGTH: 223

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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-160-61

Query Match      100.0%; Score 1204; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 5.3e-119;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGWTRLVTAALLGLMMVVTGDDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
Db 1 MGWTRLVTAALLGLMMVVTGDDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
Qy 61 VPCNNYRQKITSWMEPIVKFPGAVDGYATILVMVDPDAPSAEPRQRFWRHVLVTDIKG 120
Db 61 VPCNNYRQKITSWMEPIVKFPGAVDGYATILVMVDPDAPSAEPRQRFWRHVLVTDIKG 120
Qy 121 ADLKGKIQGQELSAQAPSPAHSGFHYQFFVYLQEGKVISLLPKENKTRGSKWMDRF 180
Db 121 ADLKGKIQGQELSAQAPSPAHSGFHYQFFVYLQEGKVISLLPKENKTRGSKWMDRF 180
Qy 181 LNRHFLGPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTROR 223
Db 181 LNRHFLGPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTROR 223
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RESULT 10
US-10-338-232
; Sequence 232, Application US/10230338
; Publication No. US20030044934A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C92
; CURRENT APPLICATION NUMBER: US/10/230,338
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 232
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-338-232
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Query Match      100.0%; Score 1204; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 5.3e-119;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGWTRLVTAALLGLMMVVTGDDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
Db 1 MGWTRLVTAALLGLMMVVTGDDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
Qy 61 VPCNNYRQKITSWMEPIVKFPGAVDGYATILVMVDPDAPSAEPRQRFWRHVLVTDIKG 120
Db 61 VPCNNYRQKITSWMEPIVKFPGAVDGYATILVMVDPDAPSAEPRQRFWRHVLVTDIKG 120
Qy 121 ADLKGKIQGQELSAQAPSPAHSGFHYQFFVYLQEGKVISLLPKENKTRGSKWMDRF 180
Db 121 ADLKGKIQGQELSAQAPSPAHSGFHYQFFVYLQEGKVISLLPKENKTRGSKWMDRF 180
Qy 181 LNRHFLGPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTROR 223
Db 181 LNRHFLGPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTROR 223
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RESULT 11
US-10-218-631-232
; Sequence 232, Application US/10218631
; Publication No. US20030045687A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C14
; CURRENT APPLICATION NUMBER: US/10/218,631
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 232
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-631-232
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Query Match      100.0%; Score 1204; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 5.3e-119;
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Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGMTMLRVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
Db 1 MGMTMLRVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
Qy 61 VPCNNYRQKITSMWEPVIFKPGAVDGTATYLVWVDPDAPRAEPQRFWRHMLVTDIKG 120
Db 61 VPCNNYRQKITSMWEPVIFKPGAVDGTATYLVWVDPDAPRAEPQRFWRHMLVTDIKG 120
Qy 121 ADLKGKIQOQELSAVQAPSPPAHSGFHRQFFVYLQEGKVI SILLPKENKTRGSWKMDRF 180
Db 121 ADLKGKIQOQELSAVQAPSPPAHSGFHRQFFVYLQEGKVI SILLPKENKTRGSWKMDRF 180
Qy 181 LNRPHLGEPEASTQFTQNTQDSPTLQAPRGRASEPKHKTRQR 223
Db 181 LNRPHLGEPEASTQFTQNTQDSPTLQAPRGRASEPKHKTRQR 223

RESULT 12
US-10-035-958-61
; Sequence 61, Application US/10035958
; Publication No. US20030049733A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Easton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C7
; CURRENT APPLICATION NUMBER: US/10/035,958
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
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; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114140
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115552
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/125774
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125778
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125826
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; PRIOR FILING DATE: 1999-04-27
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; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
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; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
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; PRIOR FILING DATE: 2001-03-22
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; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,927
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
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; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
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; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
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; SEQ ID NO 61
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-035-958-61

Query Match      100.0%; Score 1204; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 5.3e-119; Indels 0; Gaps 0;
Matches 223; Conservative 0; Mismatches 0;

QY 1 MGMTMLVTAALLGLMMVVTGDEDNSSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKV 60
Db 1 MGMTMLVTAALLGLMMVVTGDEDNSSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKV 60

QY 61 VPCNNYRQKITSWMSEPIVKFPGAVDGTATYLVNVDPDAPSRAEPRQRFWRHLVTDIKG 120
Db 61 VPCNNYRQKITSWMSEPIVKFPGAVDGTATYLVNVDPDAPSRAEPRQRFWRHLVTDIKG 120

QY 121 ADLKGKIOGOELSAOAPSPPAHSGFHRVQFFVYLQEGKVISLLPKENKTRGSKWMDRF 180
Db 121 ADLKGKIOGOELSAOAPSPPAHSGFHRVQFFVYLQEGKVISLLPKENKTRGSKWMDRF 180

QY 181 LNRFHGLGEPEASTQFTQNTQYQDSPTLQAPRGRASEPKHKTRQR 223
Db 181 LNRFHGLGEPEASTQFTQNTQYQDSPTLQAPRGRASEPKHKTRQR 223

RESULT 13
US-10-036-150-61
; Sequence 61, Application US/10036150
; Publication No. US20030049734A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2030R1C9
; CURRENT APPLICATION NUMBER: US/10/036,150
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114140
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115552
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116843
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; PRIOR APPLICATION NUMBER: 60/125774
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125778
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125826
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/127035
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/127706
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/129122
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/130359
; PRIOR FILING DATE: 1999-04-21
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; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/132379
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/132383
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/135750
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/138166
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; PRIOR APPLICATION NUMBER: 60/146970
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
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; PRIOR APPLICATION NUMBER: 09/380142
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; PRIOR APPLICATION NUMBER: 09/816744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
```


; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 246

; SEQ ID NO 232

; LENGTH: 223

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-232-224-232

Query Match 100.0%; Score 1204; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 5.3e-119;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGMTMLRVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCQGLEVFYPPELGNIGCKV 60

Db 1 MGMTMLRVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCQGLEVFYPPELGNIGCKV 60

Qy 61 VPDCNNYRQKITSMMEPIVKFPGAVDGTATYILVMVDPDAPSPRAEPQRQFWRHVLVTDIKG 120

Db 61 VPDCNNYRQKITSMMEPIVKFPGAVDGTATYILVMVDPDAPSPRAEPQRQFWRHVLVTDIKG 120

Qy 121 ADLKKGKIQGOELSAVOAPSPRAHSGFHRVYQFFVYLQEGKVISLLPKENKTRGSKWMDRF 180

Db 121 ADLKKGKIQGOELSAVOAPSPRAHSGFHRVYQFFVYLQEGKVISLLPKENKTRGSKWMDRF 180

Qy 181 LNRFLGPEPEASTQFMNTQYQDSPTLQAPRGRASEPKHKTRQ 223

Db 181 LNRFLGPEPEASTQFMNTQYQDSPTLQAPRGRASEPKHKTRQ 223

Search completed: January 30, 2005, 17:11:24
Job time : 138 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 30, 2005, 15:42:59 ; Search time 86 Seconds

(without alignments)

930.193 Million cell updates/sec

Title: US-10-035-958-61

Perfect score: 1204

Sequence: 1 MGWTELVTAALLGLLMVV.....PTLQAPRGASEPKHKTRQR 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1204	100.0	223	3	ABJ18923
2	1204	100.0	223	5	AAU83707
3	1204	100.0	223	5	ABU84969
4	1204	100.0	223	5	ABU95575
5	1204	100.0	223	6	ABU69117
6	1204	100.0	223	6	ABU80854
7	1204	100.0	223	6	ABU33820
8	1204	100.0	223	6	ABU33820
9	1204	100.0	223	6	ABU69094
10	1204	100.0	223	6	ABU82163
11	1204	100.0	223	6	ABU81558
12	1204	100.0	223	6	ADA76586
13	1204	100.0	223	6	ABJ72343
14	1204	100.0	223	6	ABJ72471
15	1204	100.0	223	6	ABO34366
16	1204	100.0	223	7	ABO25141
17	1204	100.0	223	7	ABJ72173
18	1204	100.0	223	7	ADB83722
19	1204	100.0	223	7	ADB80828
20	1204	100.0	223	7	ADB73369
21	1204	100.0	223	7	ADB78451
22	1204	100.0	223	7	ADB85099
23	1204	100.0	223	7	ADB78205
24	1204	100.0	223	7	ADB87271
25	1204	100.0	223	7	ADB84853

26	1204	100.0	223	7	ADB83968	Novel hum
27	1204	100.0	223	7	ADB73123	Novel hum
28	1204	100.0	223	7	AAE39111	Human PRO
29	1204	100.0	223	7	AAE39048	Human PRO
30	1204	100.0	223	7	ADC36961	Human PRO
31	1204	100.0	223	7	ADC21951	Human PRO
32	1204	100.0	223	7	ADC29817	Novel hum
33	1204	100.0	223	7	ADC49982	Novel hum
34	1204	100.0	223	7	ADC49181	Novel hum
35	1204	100.0	223	7	ADC49698	Novel hum
36	1204	100.0	223	7	ADC47559	Novel hum
37	1204	100.0	223	7	ADC47304	Novel hum
38	1204	100.0	223	7	ADC78179	Novel hum
39	1204	100.0	223	7	ADD06414	Novel hum
40	1204	100.0	223	7	ADD10595	Human sec
41	1204	100.0	223	7	ADD11555	Human sec
42	1204	100.0	223	7	ADD50896	Novel hum
43	1204	100.0	223	7	ADD51142	Novel hum
44	1204	100.0	223	7	ADD51142	Novel hum
45	1204	100.0	223	7	ADD37348	Human sec
46	1204	100.0	223	7	ADD50623	Human PRO
47	1204	100.0	223	7	ADD50377	Human PRO
48	1204	100.0	223	7	ADD51388	Novel hum
49	1204	100.0	223	8	ADC48935	Novel hum
50	1204	100.0	223	8	ADE21106	Novel hum
51	1204	100.0	223	8	ADE05950	Human PRO
52	1204	100.0	223	8	ADD75179	Human PRO
53	1204	100.0	223	8	ADD75925	Novel hum
54	1204	100.0	223	8	ADD85157	Novel hum
55	1204	100.0	223	8	ADD86983	Novel hum
56	1204	100.0	223	8	ADE20860	Novel hum
57	1204	100.0	223	8	ADE39157	Novel hum
58	1204	100.0	223	8	ADE05704	Human PRO
59	1204	100.0	223	8	ADD73689	Human PRO
60	1204	100.0	223	8	ADD78529	Novel hum
61	1204	100.0	223	8	ADE41556	Human sec
62	1204	100.0	223	8	ADE21352	Novel hum
63	1204	100.0	223	8	ADD77467	Novel hum
64	1204	100.0	223	8	ADE20614	Novel hum
65	1204	100.0	223	8	ADD75679	Human PRO
66	1204	100.0	223	8	ADD74195	Human PRO
67	1204	100.0	223	8	ADD74441	Human PRO
68	1204	100.0	223	8	ADD76171	Novel hum
69	1204	100.0	223	8	ADD85663	Novel hum
70	1204	100.0	223	8	ADE05212	Human PRO
71	1204	100.0	223	8	ADD75425	Human PRO
72	1204	100.0	223	8	ADD76969	Novel hum
73	1204	100.0	223	8	ADD86737	Novel hum
74	1204	100.0	223	8	ADD78205	Novel hum
75	1204	100.0	223	8	ADD77713	Novel hum
76	1204	100.0	223	8	ADD77959	Novel hum
77	1204	100.0	223	8	ADD85417	Novel hum
78	1204	100.0	223	8	ADD73949	Human PRO
79	1204	100.0	223	8	ADD74687	Human PRO
80	1204	100.0	223	8	ADD77215	Novel hum
81	1204	100.0	223	8	ADD85909	Novel hum
82	1204	100.0	223	8	ADE05458	Human PRO
83	1204	100.0	223	8	ADD74933	Human PRO
84	1204	100.0	223	8	ADF09260	Human sec
85	1204	100.0	223	8	ADG05745	Novel hum
86	1204	100.0	223	8	ADG27299	Human PRO
87	1204	100.0	223	8	ADG11362	Novel hum
88	1204	100.0	223	8	ADG12141	Novel hum
89	1204	100.0	223	8	ADF94698	Novel hum
90	1204	100.0	223	8	ADG06794	Human PRO
91	1204	100.0	223	8	ADH39138	Novel hum
92	1204	100.0	223	8	ADH43739	Human PRO
93	1204	100.0	223	8	ADG34228	Novel hum
94	1204	100.0	223	8	ADI33698	Human PRO
95	1204	100.0	223	8	ADH69792	Human PRO
96	1204	100.0	223	8	ADI29953	Novel hum
97	1204	100.0	223	8	ADM27350	Novel hum
98	1204	100.0	223	8	ADK83084	Human PRO

99	1204	100.0	223	8	ADK66708	Adk66708	Human	PRO	172	202.5	16.8	172	5	AAE25750	Aae25750	Soybean F
100	1200	99.7	223	4	AAU14138	Aau14138	Human	nov	173	202	16.8	140	7	ADJ68454	Adj68454	Human
101	1196	99.3	223	8	ADJ34902	Adj34902	Cardiovas		174	194.5	16.2	180	5	AAE25753	Aae25753	Wheat FT
102	1181	98.1	227	3	AAU94263	Aau94263	Human	pho	175	193	16.0	158	5	AAE25759	Aae25759	Corn FT h
103	1181	98.1	227	8	ADK88999	Adk88999	Human	pho	176	193	16.0	180	5	AAE25735	Aae25735	Garden ba
104	1181	98.1	227	8	ADK70502	Adk70502	Respirato		177	192.5	16.0	173	4	AAE25735	Aae25735	Mouse pab
105	1178	97.8	227	2	ADK68202	Adk68202	Novel	NOV	178	192	15.9	180	5	AAE25739	Aae25739	Corn FT h
106	1177	97.8	227	2	AAK35976	Aay35976	Extended		179	190	15.8	169	5	ABP69361	Abp69361	Human pol
107	1177	97.8	227	3	AAK64647	Aay64647	Human	pho	180	186.5	15.5	179	4	ABE62918	Abbe62918	Drosophil
108	1177	97.8	227	3	AAK00016	Aag00016	Human	sec	181	185.5	15.4	174	5	AAE25734	Aae25734	Balsam pe
109	1177	97.8	227	4	AAK88590	Aab88590	Human	hyd	182	185	15.4	178	8	ADN94938	Adn94938	Japanese
110	1177	97.8	227	8	ADP19284	Adp19284	Human	sec	183	183	15.2	178	8	ADN94935	Adn94935	Indian ri
111	1177	97.8	227	8	ADG76149	Adg76149	Human	NOV	184	182	15.1	175	3	AAE25741	Aae25741	Arabidops
112	1174	97.5	227	7	ADK68204	Adk68204	Novel	NOV	185	182	15.1	177	5	AAE25741	Aae25741	Corn FT h
113	1173	97.4	227	4	AAK48368	Aab48368	Human	SEC	186	182	15.1	179	5	AAE24557	Aae24557	Floral de
114	1173	97.4	227	7	ADG76145	Adg76145	Human	NOV	187	182	15.1	179	5	ABG31338	Abg31338	Rice Hd3a
115	1173	97.4	227	8	ADJ34900	Adj34900	Cardiovas		188	182	15.1	179	5	ABG31337	Abg31337	Rice Hd3a
116	1173	97.4	227	8	ADG76147	Adg76147	Human	NOV	189	182	15.1	179	8	ADN94939	Adn94939	Indian ri
117	1171	97.3	227	3	AAK24482	Aab24482	Human	sec	190	182	15.1	179	8	ADN94940	Adn94940	Japanese
118	1170	97.2	227	7	ADG76163	Adg76163	Human	NOV	191	181.5	15.1	211	4	ABE66541	Abbe66541	Drosophil
119	1170	97.2	227	7	ADK68182	Adk68182	Novel	NOV	192	181	15.0	210	4	ABE61522	Abbe61522	Drosophil
120	1168	97.0	227	3	AAK43330	Aab43330	Human	ORF	193	179	14.9	177	8	ADL33451	Adl33451	Festuca a
121	1167	96.9	227	3	AAK68200	Adk68200	Novel	NOV	194	177.5	14.7	225	4	ABG27458	Abg27458	Novel hum
122	1166	96.8	227	7	ADK68198	Adk68198	Novel	NOV	195	175.5	14.6	174	5	AAE25760	Aae25760	Rice FT h
123	1165	96.8	227	7	ADK68192	Adk68192	Novel	NOV	196	175.5	14.6	176	4	ABE67136	Abbe67136	Drosophil
124	1163	96.6	227	7	ADK68194	Adk68194	Novel	NOV	197	169	14.0	173	5	AAE25752	Aae25752	Soybean F
125	1160	96.3	227	7	ADK68196	Adk68196	Novel	NOV	198	168.5	14.0	172	5	AAE25737	Aae25737	Corn FT h
126	1087	90.3	201	8	ADJ34903	Adj34903	Cardiovas		199	168.5	14.0	173	5	AAE25736	Aae25736	Corn FT h
127	1070	88.9	206	7	ADG76165	Adg76165	Human	NOV	200	168.5	14.0	177	5	AAE25740	Aae25740	Corn FT h
128	1068	88.7	205	7	ADG76165	Adg76165	Human	NOV	201	167.5	13.9	184	7	ADC03498	Adc03498	Rice flow
129	1068	88.7	209	7	ADK68188	Adk68188	Novel	NOV	202	166	13.8	150	5	AAE25733	Aae25733	Peruvian
130	1068	88.7	211	7	ADG76157	Adg76157	Human	NOV	203	165	13.7	174	5	AAE25738	Aae25738	Corn FT h
131	1066	88.5	206	7	ADG76151	Adg76151	Human	NOV	204	164	13.6	174	2	ABE80315	Abbe80315	CFT1. 1/2
132	1066	88.5	209	7	ADK68184	Adk68184	Novel	NOV	205	164	13.6	175	2	AAK49098	Aay49098	Amino aci
133	1064	88.4	205	8	ADJ34901	Adj34901	Cardiovas		206	164	13.6	175	3	AAE25745	Aae25745	Arabidops
134	1064	88.4	211	7	ADG76155	Adg76155	Human	NOV	207	164	13.6	175	3	AAE25745	Aae25745	Arabidops
135	1055	87.6	205	7	ADK68190	Adk68190	Novel	NOV	208	164	13.6	175	3	AAE25745	Aae25745	Arabidops
136	1055	87.6	209	7	ADK68186	Adk68186	Novel	NOV	209	164	13.6	175	5	AAE24556	Aae24556	Arabidops
137	961	79.8	182	7	ADG76159	Adg76159	Human	NOV	210	164	13.6	175	7	ADG77597	Adc77597	A.thalian
138	957	79.5	182	7	ADG76161	Adg76161	Human	NOV	211	164	13.6	175	7	ABE80318	Abbe80318	FT. 1/200
139	761	63.2	182	4	AAU14374	Aau14374	Human	nov	212	164	13.6	201	3	AAE25742	Aae25742	Arabidops
140	743.5	61.8	183	8	ADH06092	Adh06092	Human	pol	213	164	13.6	202	3	AAE25742	Aae25742	Arabidops
141	688	57.1	149	3	AAK24591	Aab24591	Human	sec	214	161	13.4	107	3	AAE25754	Aae25754	Wheat FT
142	652	54.2	121	2	AAK11860	Aay11860	Human	5'	215	161	13.4	180	5	AAE25754	Aae25754	Wheat FT
143	561.5	46.6	242	8	ADJ34940	Adj34940	Mouse	CPP	216	160	13.3	174	5	AAE25762	Aae25762	Rice FT h
144	394	32.7	86	3	AAK24597	Aab24597	Human	sec	217	158.5	13.2	176	7	ADG77635	Adc77635	A.thalia
145	394	32.7	87	3	AAK24487	Aab24487	Human	sec	218	157.5	13.1	276	6	AAE38277	Aae38277	Rice enha
146	235.5	19.6	187	2	AAK27897	Aar27897	HGMP	prot	219	154.5	12.8	173	7	ABE80317	Abbe80317	FRD1. 1/2
147	235.5	19.6	187	2	AAK49942	Aar49942	Rat	hippo	220	153	12.7	173	5	AAE25742	Aae25742	Corn FT h
148	235.5	19.6	187	7	ADP30544	Adp30544	Rat	angio	221	152	12.6	173	5	AAE25758	Aae25758	Rice cen-
149	235.5	19.6	187	7	ADP30542	Adp30542	Rat	angio	222	152	12.6	173	8	ABE80316	Abbe80316	FRD2. 1/2
150	232	19.3	105	6	AAE37272	Aae37272	Human	gen	223	152	12.6	173	8	ADN74880	Adn74880	Rice RCN1
151	231	19.2	152	3	AAK94265	Aay94265	Onchocerc		224	152	12.6	187	6	ABU89793	Abu89793	Novel hum
152	231	19.2	152	7	ADB89002	Adb89002	Onchocerc		225	152	12.6	187	6	ADCI0118	Adci0118	Human NOV
153	229	19.0	178	4	ABE62148	Abbe62148	Drosophil		226	150	12.5	107	3	AAE25754	Aae25754	Arabidops
154	225	18.7	187	5	AAE21676	Aae21676	Mouse	pho	227	150	12.5	107	3	AAE25754	Aae25754	Arabidops
155	222.5	18.5	187	4	ABE64993	Abbe64993	Drosophil		228	150	12.5	172	8	ADJ19120	Adj19120	Ma
156	218.5	18.1	186	8	ADJ34939	Adj34939	Bovine	PE	229	148.5	12.3	175	7	ABE80314	Abbe80314	SP. 1/200
157	218.5	18.1	187	4	AAK83148	Aab83148	Mouse	peb	230	148	12.3	181	2	AAE25742	Aae25742	Antirrhin
158	218.5	18.1	187	4	AAK83150	Aab83150	Mouse	peb	231	148	12.3	181	2	ABE80311	Abbe80311	CEN. 1/20
159	216.5	18.0	202	4	ABE66542	Abbe66542	Drosophil		232	147.5	12.3	172	4	AAE25742	Aae25742	Strawber
160	214	17.8	187	5	ABG30879	Abg30879	Mouse	ner	233	147.5	12.3	172	4	AAE25742	Aae25742	Strawber
161	207.5	17.2	233	5	ABP62845	Abp62845	Human	pol	234	147.5	12.3	175	7	ABE80312	Abbe80312	CFT2. 1/2
162	205	17.0	186	6	ABO14670	Abol14670	Novel	hum	235	147	12.2	163	7	ADC03392	Adc03392	Rice flow
163	205	17.0	186	8	ADJ34938	Adj34938	Human	PEB	236	147	12.2	173	4	AAE25758	Aae25758	Strawber
164	205	17.0	187	2	AAK27718	Aar27718	HGMP	prec	237	145.5	12.1	173	4	AAE25758	Aae25758	Strawber
165	205	17.0	187	2	AAK49943	Aar49943	Human	hip	238	144.5	12.0	175	7	ABE80313	Abbe80313	CFT4. 1/2
166	205	17.0	187	2	AAK64268	Aar64268	Phosphati		239	143	11.9	179	8	ADO09334	Ado09334	Novel hum
167	205	17.0	187	5	AAE21677	Aae21677	Human	pho	240	141	11.7	173	5	AAE25751	Aae25751	Soybean F
168	205	17.0	187	6	ABO14671	Abol14671	Novel	hum	241	140	11.6	173	5	AAE25748	Aae25748	Rice FT h
169	205	17.0	187	7	ADJ68662	Adj68662	Human	hea	242	140	11.6	173	5	AAE25743	Aae25743	Corn FT h
170	204.5	17.0	176	5	AAE25747	Aae25747	Rice	FT h	243	139	11.5	173	8	ADN74882	Adn74882	Rice RCN2
171	203	16.9	121	8	ADJ34941	Adj34941	Mouse	CPP	244	139	11.5	152	2	AAR15223	Aar15223	OV-16 ant

245	138	11.5	173	7	ADC03484	Adc03484 Rice flow	318	83	6.9	595	5	ABP65177	Abp65177 Hypoxia-r
246	137.5	11.4	177	2	AAW13945	Aw13945 Arabidops	319	82.5	6.9	656	8	ADN47114	Adn47114 Thermococ
247	137.5	11.4	177	7	ABB80308	Ab80308 TFL1_1/2	320	82	6.8	745	6	ABP75664	Abp75664 Human sec
248	137.5	11.4	177	7	ADC03386	Adc03386 Rice flow	321	82	6.8	917	5	ABB97464	Abb97464 Novel hum
249	135.5	11.3	174	8	ADL33461	Adl33461 Festuca a	322	82	6.8	957	7	ADN28187	Adn28187 Human MDP
250	133	11.0	178	7	ABB80310	Abb80310 BNTFL1-3	323	82	6.8	1297	4	ABB66143	Abb66143 Drosophil
251	133	11.0	178	7	ABB80309	Abb80309 BNTFL1-1	324	81.5	6.8	177	4	AGS91425	Ag91425 C glutami
252	130	10.8	128	5	AAE25744	Aae25744 Rice FT h	325	80.5	6.7	177	4	ADN72413	Adn72413 Thale cre
253	129	10.7	104	5	AAE25761	Aae25761 Rice FT h	326	80	6.6	464	8	ADQ96834	Adq96834 CrtWcrty
254	128	10.6	173	5	ABG60940	Abg60940 Novel flo	327	79.5	6.6	648	7	ADQ96834	Adq96834 CrtWcrty
255	128	10.6	173	5	ABG60933	Abg60933 Novel flo	328	79.5	6.6	1042	6	ABU33994	Abu33994 Protein e
256	128	10.6	173	5	ABG60925	Abg60925 Novel flo	329	79	6.6	234	2	ABU33994	Abu33994 Protein e
257	124	10.3	23	3	AAE24593	Aae24593 Human sec	330	78.5	6.5	83	3	ABU33994	Abu33994 Protein e
258	121	10.0	24	3	AAE24592	Aae24592 Human sec	331	78.5	6.5	83	3	ABU33994	Abu33994 Protein e
259	120.5	10.0	136	7	ADC77598	Adc77598 A.thalian	332	78	6.5	279	7	ADF58937	Adf58937 Human pol
260	119	9.9	22	8	AD134916	Adi134916 Human CPP	333	78	6.5	354	3	AG45536	Ag45536 Arabidops
261	119	9.9	22	8	AD134918	Adi134918 Human CPP	334	78	6.5	406	3	AG45535	Ag45535 Arabidops
262	119	9.9	22	8	AD134926	Adi134926 Human CPP	335	78	6.5	454	3	AG45534	Ag45534 Arabidops
263	119	9.9	22	8	AD134921	Adi134921 Human CPP	336	78	6.5	454	5	ABB91430	Abb91430 Herbicida
264	119	9.9	22	8	AD134911	Adi134911 Human CPP	337	78	6.5	454	8	ADN73975	Adn73975 Thale cre
265	119	9.9	22	8	AD134917	Adi134917 Human CPP	338	78	6.5	875	2	AAW37098	Aw37098 Murine en
266	119	9.9	22	8	AD134907	Adi134907 Cardiov	339	77.5	6.4	1062	8	ADQ62812	Adq62812 Pseudom
267	119	9.9	22	8	AD134924	Adi134924 Human CPP	340	77	6.4	232	2	AAW37098	Aw37098 Murine en
268	119	9.9	22	8	AD134925	Adi134925 Human CPP	341	77	6.4	110	2	AAW37098	Aw37098 Murine en
269	119	9.9	22	8	AD134930	Adi134930 Human CPP	342	77	6.4	354	3	AAW37098	Aw37098 Murine en
270	119	9.9	105	5	AAE25745	Aae25745 Rice FT h	343	77	6.4	407	3	AAW37098	Aw37098 Murine en
271	118.5	9.8	82	4	ABG27456	Abg27456 Novel hum	344	77	6.4	455	3	AAW37098	Aw37098 Murine en
272	115	9.6	22	8	AD134928	Adi134928 Human CPP	345	77	6.4	455	3	AAW37098	Aw37098 Murine en
273	115	9.6	22	8	AD134922	Adi134922 Human CPP	346	77	6.4	579	5	AAE16566	Aae16566 Human int
274	115	9.6	22	8	AD134920	Adi134920 Human CPP	347	77	6.4	579	5	AAE16566	Aae16566 Human int
275	115	9.6	22	8	AD134927	Adi134927 Human CPP	348	77	6.4	602	8	ADG22680	Adg22680 Cyanophag
276	115	9.6	22	8	AD134905	Adi134905 Cardiov	349	76.5	6.4	1275	6	ABJ25467	Abj25467 Aspergill
277	113.5	9.4	197	5	ABJ04703	Abj04703 Mycobacte	350	76.5	6.4	21	3	AAW37098	Aw37098 Murine en
278	111.5	9.3	230	4	AAU30772	Aau30772 Novel hum	351	76.5	6.4	168	4	ABW98242	Abw98242 Sunflower
279	106	8.8	20	3	AAW24594	Aw24594 Human sec	352	76.5	6.4	168	5	ABW98242	Abw98242 Sunflower
280	103	8.6	409	4	ABB68134	Abb68134 Drosophil	353	76.5	6.4	321	3	AAW92341	Aw92341 Human can
281	100	8.3	173	7	ADC03372	Adc03372 Rice flow	354	76.5	6.4	1137	4	ABB61503	Abb61503 Drosophil
282	95	7.9	201	5	ABO4704	Abj04704 Mycobacte	355	76	6.3	312	7	ADH24087	Adh24087 Protein s
283	93	7.7	229	7	ABO61017	Abj061017 Klebsiell	356	76	6.3	312	8	ADH36188	Adh36188 Chemical
284	92.5	7.7	172	5	ABB98239	Abb98239 Wheat SCI	357	76	6.3	312	8	ADG93887	Adg93887 Nitrilase
285	91.5	7.6	176	5	ABB98237	Abb98237 Maize SCI	358	76	6.3	312	8	ADG93887	Adg93887 Nitrilase
286	91	7.6	17	3	AAW24595	Aw24595 Human sec	359	76	6.3	312	8	ADG93887	Adg93887 Nitrilase
287	90	7.5	179	8	ADK16367	Adk16367 Nanoarcha	360	76	6.3	351	6	ABM69090	Abm69090 Phototrab
288	89.5	7.4	120	2	AAW11503	Aw11503 Human 5'	361	76	6.3	351	6	ABM69090	Abm69090 Phototrab
289	89.5	7.4	176	2	AAW72901	Aw72901 Mycobacte	362	76	6.3	748	7	ADD47825	Add47825 Rat Prote
290	89.5	7.4	176	2	AAW21918	Aw21918 Amino aci	363	76	6.3	748	7	ADD47829	Add47829 Rat Prote
291	89.5	7.4	196	4	AAW95630	Aw95630 Human pro	364	76	6.3	1430	4	ABB64097	Abb64097 Drosophil
292	89.5	7.4	196	7	ADJ70364	Adj70364 Human hea	365	75.5	6.3	1435	6	ABJ26067	Abj26067 Aspergill
293	89.5	7.4	348	4	AAW39921	Aaw39921 Human pol	366	75.5	6.3	159	7	ABO66653	Ab666653 Klebsiell
294	89.5	7.4	380	4	AAW47132	Aaw47132 CDIFF-13	367	75.5	6.3	965	7	ADJ69650	Adj69650 Human hea
295	89.5	7.4	380	5	ABP57772	Abp57772 Tumour su	368	75.5	6.3	1049	2	AAW11576	Aaw11576 Human pho
296	89.5	7.4	389	4	AAW41707	Aaw41707 Human pol	369	75.5	6.3	1050	2	AAW11576	Aaw11576 Human pho
297	89.5	7.4	1945	4	ABW65449	Abw65449 Drosophil	370	75.5	6.3	1075	8	ADH68167	Adh68167 HA epitop
298	88.5	7.4	174	5	ABB98238	Abb98238 Maize SCI	371	75.5	6.3	1101	2	AAW23947	Aw23947 Human pho
299	88	7.3	87	5	AAE25749	Aae25749 Rice FT h	372	75.5	6.3	1101	2	AAW23947	Aw23947 Human pho
300	88	7.3	167	5	AAE25749	Aae25749 Rice FT h	373	75.5	6.3	1101	2	AAW23947	Aw23947 Human pho
301	88	7.3	174	7	ADJ59552	Adj59552 Human Pro	374	75.5	6.3	1101	5	AAU09689	Aau09689 Human p12
302	88	7.3	174	7	ADJ59552	Adj59552 Human Pro	375	75.5	6.3	1102	7	ADJ69536	Adj69536 Human hea
303	88	7.3	267	3	AAW25731	Aaw25731 Human sec	376	75.5	6.3	1102	8	ADM96267	Adm96267 Human pho
304	88	7.3	267	3	AAW25731	Aaw25731 Human sec	377	75.5	6.3	1110	8	ADH68165	Adh68165 HA epitop
305	88	7.3	297	6	ADA56855	Ada56855 Human sec	378	75.5	6.3	1639	3	AAW51134	Aaw51134 Arabidops
306	88	7.3	297	6	ADA56855	Ada56855 Human sec	379	75.5	6.3	1689	3	AAW51134	Aaw51134 Arabidops
307	87.5	7.3	1705	6	ADA47075	Ada47075 Human sec	380	75.5	6.3	2035	5	ABG79533	Abg79533 Human tum
308	87	7.2	89	8	AAU52348	Aau52348 Protein r	381	75	6.2	164	8	ABO60571	Ab60571 Human gen
309	87	7.2	163	4	AAU52348	Aau52348 Protein r	382	75	6.2	299	5	ABP39322	Abp39322 Staphyloc
310	87	7.2	163	6	ABW51897	Abw51897 Propionib	383	75	6.2	410	7	ADC96439	Adc96439 E. faeciu
311	87	7.2	165	5	ABB98240	Abb98240 Wheat SCI	384	75	6.2	651	8	ADJ35052	Adj35052 Xylanase
312	86.5	7.2	156	2	AAW37418	Aaw37418 Amino aci	385	75	6.2	670	2	AAW34517	Aaw34517 Porphyrom
313	85.5	7.1	173	7	ADW03940	Adw03940 Human pro	386	75	6.2	702	5	AAW34390	Aw34390 Porphyrom
314	85	7.1	165	5	ABB98241	Abb98241 Wheat SCI	387	75	6.2	980	2	ABG93037	Abg93037 S. cerevi
315	84	7.0	182	8	ADN46681	Adn46681 Thermococ	388	75	6.2	980	6	ABW52844	Abw52844 Protein s
316	83.5	6.9	275	3	AAW43849	Aaw43849 Human can	389	75	6.2	980	7	ADK62288	Adk62288 Disease t
317	83	6.9	595	3	AAW43303	Aaw43303 Human ORP	390	75	6.2	1419	4	ABB71134	Abb71134 Drosophil

391	74.5	6.2	236	3	AAV56286	HCAT1 c10	464	72.5	6.0	405	4	AAW39753	Human pol
392	74.5	6.2	426	7	ADH8873	Enterococ	465	72.5	6.0	408	5	ABB89459	Human pol
393	74.5	6.2	490	3	AAV56637	hCAT1 bin	466	72.5	6.0	430	4	AAW41539	Human pol
394	74.5	6.2	658	2	AAV22164	Human TIG	467	72.5	6.0	437	4	AB93745	Human pro
395	74.5	6.2	686	5	AAV14128	Human int	468	72.5	6.0	731	7	ADJ71063	Human hea
396	74.5	6.2	686	5	AAV14128	Human int	469	72.5	6.0	1009	4	ABG20820	Novel hum
397	74.5	6.2	686	5	ABP43986	Receptor	470	72.5	6.0	1047	8	ADP30309	Human sec
398	74.5	6.2	686	7	ADP31955	Human int	471	72.5	6.0	1102	2	AAW23948	Porcine p
399	74.5	6.2	1036	5	AB348686	Listeria	472	72.5	6.0	1102	2	AAW90083	Porcine G
400	74.5	6.2	1511	4	AB561693	Drosophil	473	72.5	6.0	1102	2	AAV76802	Pig p120
401	74	6.1	233	2	AAV30777	PH52-9.0	474	72.5	6.0	1102	6	ABU09753	Human pho
402	74	6.1	319	6	AB49425	Listeria	475	72.5	6.0	1192	2	AAV23899	Human res
403	74	6.1	319	6	ABU32491	Protein e	476	72.5	6.0	1211	2	AAW24560	Presenili
404	74	6.1	339	4	AAW92278	Human dig	477	72.5	6.0	1211	3	AAV23236	Human p00
405	74	6.1	504	5	ADJ17327	Polypepti	478	72.5	6.0	1211	5	ABE79001	Human p00
406	74	6.1	548	2	AAV06927	C. albica	479	72.5	6.0	2727	4	ABE61674	Drosophil
407	74	6.1	548	5	ABG93358	C. albica	480	72	6.0	84	5	ABP08420	Human ORF
408	74	6.1	548	5	ABG933261	C. albica	481	72	6.0	252	6	ABR41599	Human DIT
409	74	6.1	2038	5	AAE25098	Human kin	482	72	6.0	275	6	ABU27796	Protein e
410	74	6.1	2092	7	ABW78990	Modifie	483	72	6.0	276	7	ADD90726	Synechoc
411	74	6.1	2092	7	ADJ70161	Human hea	484	72	6.0	379	8	ABO59304	Human gen
412	74	6.1	2247	7	ADP13933	Human end	485	72	6.0	396	7	ABO73412	Pseudomon
413	74	6.1	2383	7	ADP13934	Human end	486	72	6.0	463	3	AAW41753	Arabidops
414	74	6.1	2429	5	AAE21713	Human PKI	487	72	6.0	493	3	AAW41752	Arabidops
415	74	6.1	2429	7	ABW78989	Modifie	488	72	6.0	600	3	AAW41751	Arabidops
416	73.5	6.1	244	6	ADA35146	Acinetoba	489	72	6.0	633	3	AAV52700	Pleurotus
417	73.5	6.1	429	5	ADJ16909	Human NOV	490	72	6.0	1104	6	ABR53095	Protein s
418	73.5	6.1	503	2	AAW49909	Signal re	491	72	6.0	1104	7	ADK63000	Disease t
419	73.5	6.1	503	2	AAW40481	Human SHP	492	72	6.0	1554	5	AB977332	Novel hum
420	73.5	6.1	503	2	AAU79036	Human SHP	493	72	6.0	1908	4	ABR70137	Drosophil
421	73.5	6.1	503	5	ADJ16906	Human NOV	494	71.5	5.9	113	5	ABF06540	Human ORF
422	73.5	6.1	503	6	ABU89765	Protein d	495	71.5	5.9	184	4	ABR70680	Drosophil
423	73.5	6.1	503	7	ADP56369	Human Pro	496	71.5	5.9	235	3	AAW57785	Arabidops
424	73.5	6.1	504	7	ADJ16905	Human NOV	497	71.5	5.9	235	3	AAW57786	Arabidops
425	73.5	6.1	504	7	ADD45286	Human Pro	498	71.5	5.9	235	3	AAW55516	Arabidops
426	73.5	6.1	504	7	ADJ70379	Human hea	499	71.5	5.9	302	3	AAW57791	Arabidops
427	73.5	6.1	504	8	ADM67213	Human hom	500	71.5	5.9	302	3	AAW55515	Arabidops
428	73.5	6.1	504	8	ADL83046	Human PRO	501	71.5	5.9	408	3	AAW57790	Arabidops
429	73.5	6.1	558	4	ABBS8921	Drosophil	502	71.5	5.9	413	3	AAW57789	Arabidops
430	73.5	6.1	693	4	ABBS8920	Drosophil	503	71.5	5.9	421	2	AAW93388	S. erythra
431	73.5	6.1	816	4	ABG06343	Novel hum	504	71.5	5.9	421	2	AAW96815	A. thalia
432	73.5	6.1	816	7	ADG09996	Novel pro	505	71.5	5.9	422	3	AAW59392	Arabidops
433	73.5	6.1	1103	7	ADK40897	Novel hum	506	71.5	5.9	455	3	AAW59392	Arabidops
434	73.5	6.1	1388	6	ABJ38696	Human nuc	507	71.5	5.9	486	3	AAW59391	Arabidops
435	73.5	6.1	1388	7	ADJ69333	Human hea	508	71.5	5.9	511	6	ABU07707	Human ank
436	73	6.1	458	3	AAV81990	Chimeric	509	71.5	5.9	530	3	AAW59390	Arabidops
437	73	6.1	458	7	ADC51244	P. pseudo	510	71.5	5.9	560	4	ABG00470	Novel hum
438	73	6.1	458	7	ADC51236	P. pseudo	511	71.5	5.9	560	4	ABG00470	Novel hum
439	73	6.1	508	6	ABJ25939	Aspergill	512	71.5	5.9	575	2	AAW58856	C. acidiv
440	73	6.1	508	6	ABJ25842	Aspergill	513	71.5	5.9	725	2	AAW38834	Neisseria
441	73	6.1	585	7	ADP76102	Hyperther	514	71.5	5.9	725	6	ABP77503	N. gonorr
442	73	6.1	602	6	AAO16436	Human nuc	515	71.5	5.9	725	6	ABU37822	Protein e
443	73	6.1	654	8	ADP87635	Human NOV	516	71.5	5.9	725	6	ABU37447	Protein e
444	73	6.1	654	8	ADP87627	Human NOV	517	71.5	5.9	725	6	ABU37447	Rabbit ad
445	73	6.1	660	8	ADP87637	Human NOV	518	71.5	5.9	774	4	AAU29336	Novel mar
446	73	6.1	660	8	ADP87631	Human NOV	519	71.5	5.9	774	6	AAU15308	Novel mar
447	73	6.1	661	8	ADP87629	Human NOV	520	71.5	5.9	816	4	ABG03507	Novel hum
448	73	6.1	661	8	ADP87633	Human NOV	521	71.5	5.9	861	4	ABG03507	Novel hum
449	73	6.1	747	7	ADJ68732	Human hea	522	71.5	5.9	861	4	ABG03507	Novel hum
450	73	6.1	747	8	ADM32868	Protein s	523	71	5.9	111	6	ABW73218	Staphyloc
451	73	6.1	747	8	ADQ18475	Human sof	524	71	5.9	190	7	ADH86948	Enterococ
452	73	6.1	747	8	ADP87621	Human NOV	525	71	5.9	283	5	ABG99173	Human end
453	73	6.1	748	8	ADP87625	Human NOV	526	71	5.9	283	8	ADJ83831	HERV-K HM
454	73	6.1	751	8	ADP87623	Human NOV	527	71	5.9	316	6	ABU29132	Protein e
455	73	6.1	1711	2	AAW70506	Osteocyt	528	71	5.9	316	6	ABU29132	Protein e
456	73	6.1	1711	2	AAW70507	Mutant os	529	71	5.9	389	7	ABO61502	Klebsiell
457	73	6.1	1711	5	ABR52349	Protein r	530	71	5.9	389	7	ABO61502	Klebsiell
458	73	6.1	1813	4	ABG02232	Novel hum	531	71	5.9	659	6	ABU30576	Protein e
459	72.5	6.0	214	6	ABU34042	Protein e	532	71	5.9	755	4	ABG10523	Novel hum
460	72.5	6.0	327	3	AAV83092	F-box pro	533	71	5.9	860	3	AAW23271	Pseudomon
461	72.5	6.0	327	4	ABW35162	Human Skp	534	71	5.9	930	4	ABG10524	Novel hum
462	72.5	6.0	327	5	AAO22478	Human F-b	535	71	5.9	1498	7	ADL14037	Human src
463	72.5	6.0	379	5	ABP41675	Human ova	536	71	5.9	1498	8	ADQ19580	Human sof

537	71	5.9	1944	6	AAE36107	Human chr	610	69.5	5.8	423	5	ABP73343	Candida a
538	71	5.9	1944	7	ADI26773	Human CHD	611	69.5	5.8	438	2	AAR33772	Potato tu
539	71	5.9	1944	7	ADI26772	Human CHD	612	69.5	5.8	537	7	ADD27712	Human adi
540	71	5.9	1944	7	ADJ68739	Human hea	613	69.5	5.8	588	6	ABU29418	Protein e
541	71	5.9	2000	7	ADI26747	Human GS-	614	69.5	5.8	681	7	ABU76944	Pseudomon
542	70.5	5.9	143	7	ADF60530	Human con	615	69.5	5.8	747	8	ADP87685	Pseudomon
543	70.5	5.9	184	5	AAO15429	Human TRA	616	69.5	5.8	775	7	ADG45228	Rat AMP-a
544	70.5	5.9	184	5	ABP61464	Human NF-	617	69.5	5.8	910	5	AAU90961	Mutant Pf
545	70.5	5.9	184	6	ABR41029	Human MAP	618	69.5	5.8	1066	3	AAG49832	DMS:accep
546	70.5	5.9	184	7	ADD36175	Human TRA	619	69.5	5.8	1073	3	AAG49831	Arabidops
547	70.5	5.9	258	8	ADM90859	Human pha	620	69.5	5.8	1086	3	AAG49830	Arabidops
548	70.5	5.9	258	8	ADM90858	Human pha	621	69.5	5.8	1089	4	ABU12337	Human bon
549	70.5	5.9	368	4	ABG27323	Novel hum	622	69.5	5.8	2037	4	ABU12337	Human bon
550	70.5	5.9	394	3	AAO44449	Arabidops	623	69.5	5.8	2041	7	ADJ69345	Drosophil
551	70.5	5.9	394	7	ABO61928	Arabidops	624	69.5	5.8	2048	4	AAU40027	Human hea
552	70.5	5.9	430	4	ABB61244	Klebsiell	625	69.5	5.8	2270	7	ADJ68994	Human hea
553	70.5	5.9	532	3	AAO44448	Arabidops	626	69.5	5.8	2871	5	ABJ67596	Novel hum
554	70.5	5.9	532	8	ADN72639	Thale cre	627	69	5.7	212	2	AAU12696	Fibroblas
555	70.5	5.9	548	3	AAO44447	Arabidops	628	69	5.7	212	2	AAU40077	Human FGF
556	70.5	5.9	694	6	ABM70336	Phototrab	629	69	5.7	212	5	ABJ99132	Human fib
557	70.5	5.9	698	8	ADN46567	Thermococ	630	69	5.7	214	2	AAU43338	Completel
558	70.5	5.9	998	7	ABO81716	Pseudomon	631	69	5.7	214	2	AAU43338	Completel
559	70.5	5.9	1109	3	AAU84034	Amino aci	632	69	5.7	214	6	ABR55870	Human imm
560	70.5	5.9	1159	2	AAU01570	Protein e	633	69	5.7	214	8	ADN49727	Human imm
561	70.5	5.9	1159	2	AAU40371	Human bre	634	69	5.7	226	3	AAU48506	Arabidops
562	70.5	5.9	1164	2	AAU01571	Protein e	635	69	5.7	233	4	ABP49242	Chimeric
563	70.5	5.9	1164	2	AAU58759	Human bre	636	69	5.7	234	6	ABP55483	CJRA05 pr
564	70.5	5.9	1367	3	AAU84035	Amino aci	637	69	5.7	245	2	AAU98943	Humanised
565	70	5.8	268	7	ADC31466	Human nov	638	69	5.7	265	3	AAU48505	Arabidops
566	70	5.8	273	4	AAU32368	Novel hum	639	69	5.7	329	7	ADC23981	Protein s
567	70	5.8	309	4	AAU13671	Peptide #	640	69	5.7	329	8	ADH36082	Chemical
568	70	5.8	309	4	ABG26602	Peptide #	641	69	5.7	329	8	ADH36082	Chemical
569	70	5.8	309	4	AAU26070	Peptide #	642	69	5.7	329	8	ADI62380	Nitrilase
570	70	5.8	309	4	ABG27453	Human pep	643	69	5.7	329	8	ADI62380	Nitrilase
571	70	5.8	309	4	ABU18099	Protein #	644	69	5.7	361	7	ADP04814	Bacterial
572	70	5.8	309	4	AAU65809	Human bon	645	69	5.7	378	5	ABU93803	Herbicida
573	70	5.8	309	4	AAU53431	Human bra	646	69	5.7	378	5	ABU93803	Herbicida
574	70	5.8	309	4	ABG47455	Human liv	647	69	5.7	395	3	AAU16813	Arabidops
575	70	5.8	309	4	AAU01421	Peptide #	648	69	5.7	415	6	ADA48422	Rice prot
576	70	5.8	309	5	ABG35443	Human pep	649	69	5.7	424	3	AAU16811	Arabidops
577	70	5.8	316	4	AAU35202	Enterococ	650	69	5.7	425	4	ABG25955	Novel hum
578	70	5.8	354	4	AAU89296	Human sec	651	69	5.7	492	4	AAU31949	Amino aci
579	70	5.8	354	5	ABU08166	Human cyc	652	69	5.7	672	6	ADA54497	Human pro
580	70	5.8	354	8	ADN08302	3F3 cell	653	69	5.7	674	4	AAU92775	Human pro
581	70	5.8	359	6	ABU21164	Protein e	654	69	5.7	681	4	AAU31955	Amino aci
582	70	5.8	402	5	AAU16907	NOVX prot	655	69	5.7	762	5	ABP69032	Human pol
583	70	5.8	408	4	AAU93717	Human pol	656	69	5.7	773	2	AAU46726	Desilicoro
584	70	5.8	408	8	ADL31630	Human pro	657	69	5.7	774	2	AAU87548	A Tfu DNA
585	70	5.8	428	5	ABU06069	Human NS	658	69	5.7	818	6	AAE33689	Human str
586	70	5.8	438	3	AAU15721	Deltal30	659	69	5.7	1031	5	ADI46109	Single st
587	70	5.8	485	6	ABR40829	Zea mays	660	69	5.7	1045	7	ADB4676	Human pro
588	70	5.8	485	6	ABR40834	Zea mays	661	69	5.7	1064	4	AAU68898	Human HX2
589	70	5.8	503	5	ADI16584	Human NOV	662	69	5.7	1339	5	ABG65653	Human bre
590	70	5.8	503	8	ADN42238	Human nov	663	68.5	5.7	185	4	AAU10827	Novel hum
591	70	5.8	542	7	ADN07155	Aspergill	664	68.5	5.7	205	4	ABU12485	Human bon
592	70	5.8	542	7	ADN07042	Aspergill	665	68.5	5.7	210	4	ABU70803	Drosophil
593	70	5.8	746	6	ADP49787	Human 193	666	68.5	5.7	211	3	AAU75508	Fibroblas
594	70	5.8	763	6	ADU12177	Alloiooc	667	68.5	5.7	283	6	ABU27575	Protein e
595	70	5.8	765	6	ADU12175	Alloiooc	668	68.5	5.7	321	3	AAU94272	Corn argi
596	70	5.8	784	6	ABU38646	Protein e	669	68.5	5.7	343	3	AAU58791	Soybean p
597	70	5.8	830	6	ADA89281	Human IBD	670	68.5	5.7	343	6	ABU08363	Soybean p
598	70	5.8	836	6	ADA89279	Human IBD	671	68.5	5.7	425	8	ADN49489	Oil-assoc
599	70	5.8	1417	6	AAU23135	Protein e	672	68.5	5.7	472	2	AAW26312	Rat STCH
600	70	5.8	1839	5	ABP73768	Candida a	673	68.5	5.7	551	7	ABO67710	Klebsiell
601	70	5.8	2137	7	ADL15088	Human mal	674	68.5	5.7	605	5	AAU77947	Haloperox
602	70	5.8	2161	4	AAU78959	Human pro	675	68.5	5.7	605	5	AAU51613	Dreschler
603	70	5.8	2189	4	AAU79943	Human pro	676	68.5	5.7	860	8	ADU50127	Oil-assoc
604	70	5.8	2432	8	ADM87266	Human pro	677	68.5	5.7	1185	5	AAU80135	Chimeric
605	70	5.8	2523	4	AAU03503	Human pro	678	68.5	5.7	1185	6	AAU33407	Chimeric
606	70	5.8	2545	5	ABU98406	Human NOV	679	68.5	5.7	1879	8	ADN42338	Human nov
607	70	5.8	6797	4	AAU31558	Pimaricin	680	68	5.6	180	8	ADN47103	Thermococ
608	69.5	5.8	277	4	ABU52647	Escherich	681	68	5.6	214	2	AAU00373	Anti-CD18
609	69.5	5.8	356	4	AAU39320	Human pol	682	68	5.6	233	2	AAU22755	Reshaped

683	68	5.6	259	7	ABO82377	AbO82377 Pseudomon	756	67.5	5.6	596	2	AAR39554	Aar39554 Deduced a
684	68	5.6	328	5	ABP73902	Abp73902 Candida a	757	67.5	5.6	596	4	AAB30862	Aab30862 Amino aci
685	68	5.6	339	3	AGI18352	Aagi18352 Arabidops	758	67.5	5.6	609	4	AB92953	Ab92953 Human pro
686	68	5.6	378	3	AAQ18351	Aaq18351 Arabidops	759	67.5	5.6	609	6	ADA11709	Ada11709 Human nov
687	68	5.6	395	3	AGS4284	Aags4284 Arabidops	760	67.5	5.6	650	6	ABU11592	Abu11592 Human MDD
688	68	5.6	415	3	AGS4283	Aags4283 Arabidops	761	67.5	5.6	706	7	ADK62366	Adk62366 Disease t
689	68	5.6	424	3	AGS4282	Aags4282 Arabidops	762	67.5	5.6	774	6	ABU28129	Abu28129 Protein e
690	68	5.6	424	8	ADN72579	Adn72579 Thale cre	763	67.5	5.6	921	4	AAE05723	Aae05723 Bacillus
691	68	5.6	446	4	AAB66653	Aab66653 LPL S44YX	764	67.5	5.6	921	4	AAE05727	Aae05727 Bacillus
692	68	5.6	448	4	AAB66655	Aab66655 Pre-LPL S	765	67.5	5.6	921	4	AAE05725	Aae05725 Bacillus
693	68	5.6	449	7	ADB31773	Adb31773 Plant (A.	766	67.5	5.6	921	4	AAE05726	Aae05726 Bacillus
694	68	5.6	449	7	ADD55828	Add55828 Thalecres	767	67.5	5.6	921	4	AAE05724	Aae05724 Bacillus
695	68	5.6	449	7	ADD31075	Add31075 Plant vie	768	67.5	5.6	921	4	AAE05689	Aae05689 Bacillus
696	68	5.6	449	8	AD4141539	Adi41539 Plant tra	769	67.5	5.6	2270	2	AAE05723	Aae05723 Candida a
697	68	5.6	449	8	AD001599	Ado01599 Thalecres	770	67	5.6	157	2	AAR98836	Aar98836 CD40 asso
698	68	5.6	453	4	AAQ90523	Aaq90523 C glutami	771	67	5.6	158	2	AAR63121	Aar63121 ORF1 gene
699	68	5.6	453	4	AAQ90523	Aaq90523 C glutami	772	67	5.6	181	2	AAR98834	Aar98834 CD40 asso
700	68	5.6	458	3	AAW81989	Aaw81989 Chimeric	773	67	5.6	214	2	AAR30776	Aar30776 H52L6-158
701	68	5.6	474	2	AAW931150	Aaw931150 Thermoana	774	67	5.6	228	4	AAB07003	Aab07003 Human TRA
702	68	5.6	475	2	AAW681154	Aaw681154 Human lip	775	67	5.6	258	4	AAM40139	Aam40139 Human pol
703	68	5.6	475	2	AAW49555	Aay49555 Human pro	776	67	5.6	282	3	AAV79565	Aay79565 Human TRA
704	68	5.6	475	4	AAB66654	Aab66654 Mature LP	777	67	5.6	330	6	ABU49019	Abu49019 Protein e
705	68	5.6	475	5	ABBO63322	Abb06322 Lipoprote	778	67	5.6	337	4	ABG07578	Abg07578 Novel hum
706	68	5.6	475	7	AD56914	Ad56914 Human lip	779	67	5.6	337	4	ABG00104	Abg00104 Novel hum
707	68	5.6	475	7	ADDA48644	Add48644 Human pro	780	67	5.6	347	3	AAW04871	Aaw04871 Phosphory
708	68	5.6	475	7	ADDA46966	Add46966 Human pro	781	67	5.6	372	2	AAW04869	Aaw04869 Cyclin-de
709	68	5.6	475	7	ADDA46958	Add46958 Human pro	782	67	5.6	372	2	AAW04871	Aaw04871 Phosphory
710	68	5.6	475	7	ADE56906	Ad56906 Human pro	783	67	5.6	372	5	AAU75107	Aau75107 Cell cycl
711	68	5.6	475	7	ADDA46962	Add46962 Human pro	784	67	5.6	372	5	ABU62606	Abu62606 Human P-T
712	68	5.6	475	7	ADDE56910	Ad56910 Human pro	785	67	5.6	372	6	ADF45045	Adf45045 Human kin
713	68	5.6	506	7	ADM26514	Adm26514 Hyperther	786	67	5.6	372	8	ADH09516	Adh09516 Human hos
714	68	5.6	527	7	ADM05229	Adm05229 Human pro	787	67	5.6	372	8	ADH09517	Adh09517 Human hos
715	68	5.6	585	2	AAW37757	Aaw37757 S-region	788	67	5.6	372	8	ADH09517	Adh09517 Human hos
716	68	5.6	585	4	AAU27756	Aau27756 Human ful	789	67	5.6	372	8	ADH09521	Adh09521 Human hos
717	68	5.6	623	2	AAU38833	Aay38833 Neisseria	790	67	5.6	372	8	ADP74343	Adp74343 Human cyc
718	68	5.6	623	2	AAU38833	Aay38833 Neisseria	791	67	5.6	372	8	ADP74343	Adp74343 Human cyc
719	68	5.6	687	8	ADN99664	Adn99664 Novel hum	792	67	5.6	388	7	ADF04102	Adf04102 Bacterial
720	68	5.6	737	4	AAB67571	Aab67571 Nino aci	793	67	5.6	396	8	ADM48230	Adm48230 Polypepti
721	68	5.6	738	2	AAW95332	Aaw95332 Human pho	794	67	5.6	396	8	ADM48230	Adm48230 Polypepti
722	68	5.6	782	2	ABB40936	Abb40936 Drosophil	795	67	5.6	412	2	AAV41708	Aay41708 Human pro
723	68	5.6	868	3	AAAG46295	Aag46295 Arabidops	796	67	5.6	412	2	AAV41708	Aay41708 Human pro
724	68	5.6	870	8	ADK17029	Adk17029 Nanoarcha	797	67	5.6	412	3	ABE19579	Abi19579 Human PRO
725	68	5.6	999	3	AAAG46294	Aag46294 Arabidops	798	67	5.6	412	3	ABE19579	Abi19579 Human PRO
726	68	5.6	1032	3	AAAG45673	Aag45673 Arabidops	799	67	5.6	412	3	ABE19579	Abi19579 Human PRO
727	68	5.6	1033	4	ABG32320	Abg32320 Novel hum	800	67	5.6	412	4	AAB50954	Aab50954 Human pro
728	68	5.6	1045	3	AAAG45672	Aag45672 Arabidops	801	67	5.6	412	4	AAB50954	Aab50954 Human pro
729	68	5.6	1065	3	AAAG46293	Aag46293 Arabidops	802	67	5.6	412	5	ABG34036	Abg34036 Human pro
730	68	5.6	1468	4	ABE45671	Abb45671 Arabidops	803	67	5.6	412	6	ABO25210	Ab025210 Novel hum
731	68	5.6	1523	5	ABBO9551	Abb09551 Human set	804	67	5.6	412	6	ABO25210	Ab025210 Novel hum
732	68	5.6	1681	8	AD010061	Ado10061 Novel hum	805	67	5.6	412	6	ABU72216	Abu72216 Novel hum
733	68	5.6	1681	8	AD010061	Ado10061 Novel hum	806	67	5.6	412	6	ABU72216	Abu72216 Novel hum
734	68	5.6	1723	5	ABBO9551	Abb09551 Human set	807	67	5.6	412	6	ABU72216	Abu72216 Novel hum
735	68	5.6	1723	5	ABBO9551	Abb09551 Human set	808	67	5.6	412	6	ABU72216	Abu72216 Novel hum
736	68	5.6	1867	5	ABG66751	Abg66751 Human nov	809	67	5.6	412	6	ABU72216	Abu72216 Novel hum
737	68	5.6	1867	5	ABG66751	Abg66751 Human nov	810	67	5.6	412	6	ABU72216	Abu72216 Novel hum
738	68	5.6	1893	8	ADE28321	Ad28321 Human KPP	811	67	5.6	412	6	ADA43479	Ada43479 Human sec
739	68	5.6	1929	8	ADJ50993	Adj50993 Human nov	812	67	5.6	412	6	ADA43479	Ada43479 Human sec
740	68	5.6	2476	2	AAW67738	Aaw67738 Pig p105	813	67	5.6	412	6	ADA43479	Ada43479 Human sec
741	68	5.6	2476	2	AAW67738	Aaw67738 Pig p105	814	67	5.6	412	6	ADA43479	Ada43479 Human sec
742	67.5	5.6	120	7	ABM73703	Abm73703 DNA clone	815	67	5.6	412	6	ADA43479	Ada43479 Human sec
743	67.5	5.6	158	7	ABM73939	Abm73939 DNA clone	816	67	5.6	412	6	ADA43479	Ada43479 Human sec
744	67.5	5.6	164	6	ADA12136	Ada12136 Human nov	817	67	5.6	412	7	ADA43595	Ada43595 Human sec
745	67.5	5.6	165	2	AAV36329	Aay36329 Human nov	818	67	5.6	412	7	ADA43595	Ada43595 Human sec
746	67.5	5.6	165	6	ADA11728	Ada11728 Human nov	819	67	5.6	412	7	ADA43595	Ada43595 Human sec
747	67.5	5.6	277	6	AAU35496	Aau35496 Protein e	820	67	5.6	412	7	ADA43595	Ada43595 Human sec
748	67.5	5.6	309	3	AAU93289	Aay93289 Amino aci	821	67	5.6	412	7	ADA43595	Ada43595 Human sec
749	67.5	5.6	512	2	AAW87797	Aaw87797 Protease	822	67	5.6	412	7	ADA43595	Ada43595 Human sec
750	67.5	5.6	512	2	AAW87797	Aaw87797 Protease	823	67	5.6	412	7	ADA43595	Ada43595 Human sec
751	67.5	5.6	512	2	AAW87797	Aaw87797 Protease	824	67	5.6	412	7	ADA43595	Ada43595 Human sec
752	67.5	5.6	512	2	AAW87797	Aaw87797 Protease	825	67	5.6	412	7	ADA43595	Ada43595 Human sec
753	67.5	5.6	512	3	AAW87797	Aaw87797 Protease	826	67	5.6	412	7	ADA43595	Ada43595 Human sec
754	67.5	5.6	538	4	ABG27419	Abg27419 Novel hum	827	67	5.6	412	7	ADA43595	Ada43595 Human sec
755	67.5	5.6	550	7	ADC01233	Adc01233 Enterohae	828	67	5.6	412	7	ADA43595	Ada43595 Human sec

829	67	5.6	412	7	ADC43805	Adc43805 Human sec	902	67	5.6	412	8	ADP24116	Adf24116 Human sec
830	67	5.6	412	7	ADC61565	Adc61565 Human sec	903	67	5.6	412	8	ADF40548	Adf40548 Human sec
831	67	5.6	412	7	ADC63529	Adc63529 Human sec	904	67	5.6	412	8	ADF23492	Adf23492 Human sec
832	67	5.6	412	7	ADC66629	Adc66629 Human sec	905	67	5.6	412	8	ADF33475	Adf33475 Human sec
833	67	5.6	412	7	ADC68753	Adc68753 Human sec	906	67	5.6	412	8	ADF26942	Adf26942 Human sec
834	67	5.6	412	7	ADC62813	Adc62813 Human sec	907	67	5.6	412	8	ADF27578	Adf27578 Human sec
835	67	5.6	412	7	ADC67878	Adc67878 Human sec	908	67	5.6	412	8	ADF41172	Adf41172 Human sec
836	67	5.6	412	7	ADC41198	Adc41198 Human sec	909	67	5.6	412	8	ADF32851	Adf32851 Human sec
837	67	5.6	412	7	ADC67253	Adc67253 Human sec	910	67	5.6	412	8	ADF25217	Adf25217 Human sec
838	67	5.6	412	7	ADC23358	Adc23358 Human tra	911	67	5.6	412	8	ADF26318	Adf26318 Human sec
839	67	5.6	412	7	ADC36051	Adc36051 Human PRO	912	67	5.6	412	8	ADF34107	Adf34107 Human sec
840	67	5.6	412	7	ADC62189	Adc62189 Human sec	913	67	5.6	412	8	ADF46344	Adf46344 Human sec
841	67	5.6	412	7	ADC41822	Adc41822 Human sec	914	67	5.6	412	8	ADG11028	Adg11028 Human sec
842	67	5.6	412	7	ADE04878	Adc04878 Human PRO	915	67	5.6	412	8	ADG10912	Adg10912 Human sec
843	67	5.6	412	7	ADE11184	Adc11184 Human PRO	916	67	5.6	412	8	ADH31440	Adh31440 Human PRO
844	67	5.6	412	7	ADE49191	Adc49191 Human PRO	917	67	5.6	412	8	ADH38688	Adh38688 Human sec
845	67	5.6	412	7	ADD88115	Adc88115 Human PRO	918	67	5.6	412	8	ADH29323	Adh29323 Human sec
846	67	5.6	412	7	ADE35245	Adc35245 Human sec	919	67	5.6	412	8	ADH23626	Adh23626 Human sec
847	67	5.6	412	7	ADE16359	Adc16359 Human sec	920	67	5.6	412	8	ADH26956	Adh26956 Human sec
848	67	5.6	412	7	ADD72974	Adc72974 Human sec	921	67	5.6	412	8	ADG50330	Adg50330 Human sec
849	67	5.6	412	7	ADD95410	Adc95410 Human sec	922	67	5.6	412	8	ADH26840	Adh26840 Novel hum
850	67	5.6	412	7	ADE06340	Adc06340 Human PRO	923	67	5.6	412	8	ADH26840	Adh26840 Human sec
851	67	5.6	412	7	ADE38115	Adc38115 Human PRO	924	67	5.6	412	8	ADG49706	Adg49706 Human sec
852	67	5.6	412	7	ADD72332	Adc72332 Human sec	925	67	5.6	412	8	ADG51578	Adg51578 Human sec
853	67	5.6	412	7	ADD88231	Adc88231 Human PRO	926	67	5.6	412	8	ADH38108	Adh38108 Novel hum
854	67	5.6	412	7	ADE16983	Adc16983 Human sec	927	67	5.6	412	8	ADG49082	Adg49082 Human sec
855	67	5.6	412	7	ADD90812	Adc90812 Human sec	928	67	5.6	412	8	ADH38804	Adh38804 Human sec
856	67	5.6	412	7	ADF46997	Adf46997 Human sec	929	67	5.6	412	8	ADG48458	Adg48458 Human sec
857	67	5.6	412	7	ADF93367	Adf93367 Human sec	930	67	5.6	412	8	ADH23742	Adh23742 Human sec
858	67	5.6	412	7	ADG06460	Adg06460 Human PRO	931	67	5.6	412	8	ADH40118	Adh40118 Human PRO
859	67	5.6	412	7	ADG14400	Adg14400 Human LLP	932	67	5.6	412	8	ADH40002	Adh40002 Human PRO
860	67	5.6	412	7	ADG05411	Adg05411 Human PRO	933	67	5.6	412	8	ADH31324	Adh31324 Human PRO
861	67	5.6	412	7	ADG52754	Adg52754 Human sec	934	67	5.6	412	8	ADH29202	Adh29202 Human sec
862	67	5.6	412	7	ADG60074	Adg60074 Human sec	935	67	5.6	412	8	ADH49417	Adh49417 Novel hum
863	67	5.6	412	7	ADG82412	Adg82412 Human PRO	936	67	5.6	412	8	ADG50954	Adg50954 Human sec
864	67	5.6	412	7	ADI60834	Adi60834 Human sec	937	67	5.6	412	8	ADH51881	Adh51881 Novel hum
865	67	5.6	412	8	ADE51665	Adc51665 Human sec	938	67	5.6	412	8	ADH49736	Adh49736 Novel hum
866	67	5.6	412	8	ADE51781	Adc51781 Human sec	939	67	5.6	412	8	ADH52337	Adh52337 Novel hum
867	67	5.6	412	8	ADE37639	Adc37639 Human sec	940	67	5.6	412	8	ADG58898	Adg58898 Human sec
868	67	5.6	412	8	ADE37523	Adc37523 Human sec	941	67	5.6	412	8	ADH52453	Adh52453 Novel hum
869	67	5.6	412	8	ADD95294	Adc95294 Human sec	942	67	5.6	412	8	ADH58450	Adh58450 Novel hum
870	67	5.6	412	8	ADE37994	Adc37994 Human PRO	943	67	5.6	412	8	ADH51765	Adh51765 Novel hum
871	67	5.6	412	8	ADE76083	Adc76083 Human PRO	944	67	5.6	412	8	ADG62354	Adg62354 Human sec
872	67	5.6	412	8	ADE39406	Adc39406 Human PRO	945	67	5.6	412	8	ADH58326	Adh58326 Novel hum
873	67	5.6	412	8	ADE04210	Adc04210 Human PRO	946	67	5.6	412	8	ADI13523	Adi13523 Novel hum
874	67	5.6	412	8	ADE39807	Adc39807 Human PRO	947	67	5.6	412	8	ADH25379	Adh25379 Human neu
875	67	5.6	412	8	ADE19672	Adc19672 Human PRO	948	67	5.6	412	8	ADK00779	Adk00779 Human PRO
876	67	5.6	412	8	ADE77250	Adc77250 Human sec	949	67	5.6	412	8	ADL08520	Adl08520 Human sec
877	67	5.6	412	8	ADE65358	Adc65358 Human PRO	950	67	5.6	412	8	ADL30884	Adl30884 Human PRO
878	67	5.6	412	8	ADE48491	Adc48491 Human sec	951	67	5.6	412	8	ADM17156	Adm17156 Human sec
879	67	5.6	412	8	ADE75967	Adc75967 Human PRO	952	67	5.6	412	8	ADL06990	Adl06990 Human sec
880	67	5.6	412	8	ADE37878	Adc37878 Human PRO	953	67	5.6	463	3	AAG17339	Ag17339 Arabidops
881	67	5.6	412	8	ADE64488	Adc64488 Human PRO	954	67	5.6	463	3	AAG42685	Ag42685 Arabidops
882	67	5.6	412	8	ADE38823	Adc38823 Human PRO	955	67	5.6	465	3	AAG17338	Ag17338 Arabidops
883	67	5.6	412	8	ADE51897	Adc51897 Human sec	956	67	5.6	465	3	AAG42684	Ag42684 Arabidops
884	67	5.6	412	8	ADD90928	Adc90928 Human sec	957	67	5.6	465	5	AB992842	Ab992842 Herbicida
885	67	5.6	412	8	ADE38707	Adc38707 Human PRO	958	67	5.6	465	8	ADN74339	Adn74339 Thale cre
886	67	5.6	412	8	ADE37407	Adc37407 Human PRO	959	67	5.6	472	2	AAR98835	Aar98835 Cd40 asso
887	67	5.6	412	8	ADD06224	Adc06224 Human PRO	960	67	5.6	474	7	ADD46964	Add46964 Rat Prote
888	67	5.6	412	8	ADD90083	Adc90083 Human sec	961	67	5.6	474	7	ADD48642	Add48642 Rat Prote
889	67	5.6	412	8	ADE38591	Adc38591 Human PRO	962	67	5.6	474	7	ADG56912	Adg56912 Rat Prote
890	67	5.6	412	8	ADE39522	Adc39522 Human PRO	963	67	5.6	474	7	ADG56904	Adg56904 Rat Prote
891	67	5.6	412	8	ADD89127	Adc89127 Human PRO	964	67	5.6	474	7	ADG46960	Adg46960 Rat Prote
892	67	5.6	412	8	ADD88894	Adc88894 Human PRO	965	67	5.6	474	7	ADG46956	Adg46956 Rat Prote
893	67	5.6	412	8	ADE19788	Adc19788 Human PRO	966	67	5.6	474	7	ADG46956	Adg46956 Rat Prote
894	67	5.6	412	8	ADE77366	Adc77366 Human sec	967	67	5.6	484	8	ADJ49562	Adj49562 Oil-aseoc
895	67	5.6	412	8	ADE65242	Adc65242 Human PRO	968	67	5.6	487	3	AAG17337	Ag17337 Arabidops
896	67	5.6	412	8	ADE39290	Adc39290 Human PRO	969	67	5.6	487	3	AAG42683	Ag42683 Arabidops
897	67	5.6	412	8	ADE38475	Adc38475 Human sec	970	67	5.6	512	2	AAW27434	Aaw27434 Human CRA
898	67	5.6	412	8	ADE89592	Adc89592 Human sec	971	67	5.6	516	2	AAW27436	Aaw27436 Human CRA
899	67	5.6	412	8	ADF61232	Adf61232 Human sec	972	67	5.6	543	2	AAR98833	Aar98833 Cd40 asso
900	67	5.6	412	8	ADF39924	Adf39924 Human sec	973	67	5.6	543	2	AAW27432	Aaw27432 Human CRA
901	67	5.6	412	8	ADF45720	Adf45720 Human sec	974	67	5.6	543	6	ABO07169	Ab007169 Human p53

975	67	5.6	556	2	AAR90620	Sulfolobu	1048	66.5	5.5	2397	8	ADJ76266	Marker ge
976	67	5.6	556	2	AAR92755	Trehalose	1049	66	5.5	129	6	ABU40513	Abu40513 Protein e
977	67	5.6	567	4	AAB67615	Amino aci	1050	66	5.5	152	3	AAg41898	AAg41898 Arabidops
978	67	5.6	567	5	AAO17756	Murine CD	1051	66	5.5	163	3	AAG25841	AAG25841 Arabidops
979	67	5.6	567	5	ABBS7054	Mouse iec	1052	66	5.5	185	8	ABO59731	ABO59731 Human gan
980	67	5.6	567	7	ADD25542	Binding d	1053	66	5.5	186	3	AAg41897	AAg41897 Arabidops
981	67	5.6	568	2	AAW03146	LMP1 aso	1054	66	5.5	186	5	ABP60711	ABP60711 Arabidops
982	67	5.6	568	2	AAW27431	Human CRA	1055	66	5.5	233	7	ABO84024	ABO84024 Pseudomon
983	67	5.6	568	3	AAy98166	Human TRA	1056	66	5.5	256	5	ABG91559	ABG91559 Parine/py
984	67	5.6	568	6	AAO17757	Human CD4	1057	66	5.5	277	7	ADC97586	ADC97586 E. faeciu
985	67	5.6	568	6	ABO07171	Human p53	1058	66	5.5	296	4	AAE67329	AAE67329 Human neu
986	67	5.6	568	7	ADB80964	RING-SH c	1059	66	5.5	333	5	AAE14786	AAE14786 Human inm
987	67	5.6	568	7	ADB80957	Ring-SH c	1060	66	5.5	361	6	ABU20420	ABU20420 Protein e
988	67	5.6	634	2	AAW27435	Human CRA	1061	66	5.5	378	7	ADSO8611	ADSO8611 Novel pro
989	67	5.6	638	2	AAW27437	Human CRA	1062	66	5.5	378	7	ADSO9970	ADSO9970 Novel pro
990	67	5.6	665	2	AAW27433	Human CRA	1063	66	5.5	382	4	ABG21902	ABG21902 Novel hum
991	67	5.6	667	6	ABR56765	Human sec	1064	66	5.5	405	5	AAE30535	AAE30535 Fruit fly
992	67	5.6	678	5	ABP54948	Schizosac	1065	66	5.5	440	4	AAE85358	AAE85358 Human pho
993	67	5.6	678	7	ABU61621	Yeast MPH	1066	66	5.5	442	4	AAE94895	AAE94895 Human pro
994	67	5.6	650	2	AAW27428	Human CRA	1067	66	5.5	462	7	ABO69784	ABO69784 Pseudomon
995	67	5.6	732	4	AAE93312	Human pro	1068	66	5.5	471	5	AAO15421	AAO15421 Human gen
996	67	5.6	737	7	ADE56440	Human pro	1069	66	5.5	474	3	AAE23807	AAE23807 Arabidops
997	67	5.6	737	7	ADD45348	Human pro	1070	66	5.5	476	4	AAE95719	AAE95719 Human pro
998	67	5.6	737	8	ADO20067	Human pro	1071	66	5.5	485	6	ABU45205	ABU45205 Protein e
999	67	5.6	804	7	ADM05476	Human pro	1072	66	5.5	493	3	AAE23806	AAE23806 Arabidops
1000	67	5.6	814	6	ABU41753	Protein e	1073	66	5.5	505	4	ABE58784	ABE58784 Drosophil
1001	67	5.6	815	7	ADF28113	Murine gl	1074	66	5.5	517	4	ABG14307	ABG14307 Novel hum
1002	67	5.6	817	4	AAW79318	Human pro	1075	66	5.5	523	4	ABG26147	ABG26147 Novel hum
1003	67	5.6	817	4	AAW79319	Human pro	1076	66	5.5	524	4	ABG00694	ABG00694 Novel hum
1004	67	5.6	885	4	ABG17558	Novel hum	1077	66	5.5	524	4	ABG02795	ABG02795 Novel hum
1005	67	5.6	1216	7	ADC31455	Human nov	1078	66	5.5	524	7	ADI21621	ADI21621 Novel hum
1006	67	5.6	1682	4	ABG13667	Novel hum	1079	66	5.5	528	4	AAE95149	AAE95149 Human pro
1007	67	5.6	1682	4	ABG07239	Novel hum	1080	66	5.5	544	4	AAE93653	AAE93653 Human pro
1008	67	5.6	1883	4	ABG19121	Novel hum	1081	66	5.5	560	4	AAE95581	AAE95581 Human pro
1009	67	5.6	2002	4	ABG12556	Novel hum	1082	66	5.5	561	4	AAE94345	AAE94345 Human pro
1010	67	5.6	2294	7	ADJ68907	Human hea	1083	66	5.5	580	6	ABJ25525	ABJ25525 Aspergill
1011	67	5.6	2552	6	ABU33748	Protein e	1084	66	5.5	608	4	ABG08671	ABG08671 Novel hum
1012	66.5	5.5	180	7	AAO23186	Dye-dideo	1085	66	5.5	666	5	ABG99169	ABG99169 Human end
1013	66.5	5.5	199	5	ABP33614	Myo-inosi	1086	66	5.5	666	8	ADJ83893	ADJ83893 HERV-K HM
1014	66.5	5.5	202	5	ABP33615	Myo-inosi	1087	66	5.5	666	8	ADJ83829	ADJ83829 HERV-K HM
1015	66.5	5.5	210	4	AAW78514	Human pro	1088	66	5.5	667	8	ADJ83894	ADJ83894 HERV-K HM
1016	66.5	5.5	236	5	ABP33611	Myo-inosi	1089	66	5.5	680	6	ADJ826125	ADJ826125 Aspergill
1017	66.5	5.5	236	5	ABP33610	Myo-inosi	1090	66	5.5	709	5	ABO808645	ABO808645 Human pan
1018	66.5	5.5	238	4	AAW41606	Human pol	1091	66	5.5	710	4	AAW78335	AAW78335 Human pro
1019	66.5	5.5	238	8	ADL23055	Humanised	1092	66	5.5	710	5	AAO15420	AAO15420 Human gen
1020	66.5	5.5	239	3	AAW39820	Human pol	1093	66	5.5	710	7	ADF28105	ADF28105 Adiponec
1021	66.5	5.5	269	3	AAy94745	Murine CD	1094	66	5.5	731	3	AAy91954	AAy91954 Human cyc
1022	66.5	5.5	284	4	ABG17245	Novel hum	1095	66	5.5	731	4	AAE95828	AAE95828 Human pro
1023	66.5	5.5	284	7	ADF59550	Human pol	1096	66	5.5	737	5	ABE97192	ABE97192 Novel hum
1024	66.5	5.5	285	3	AAy58646	Human kid	1097	66	5.5	737	7	ADF76927	ADF76927 Novel hum
1025	66.5	5.5	285	3	AAy58680	Human kid	1098	66	5.5	738	8	ADM43092	ADM43092 Human PLA
1026	66.5	5.5	310	5	ABP33602	Human myo	1099	66	5.5	738	8	ADH39770	ADH39770 Streptom
1027	66.5	5.5	321	4	AAU03104	Thermococ	1100	66	5.5	743	4	AAE09851	AAE09851 Novel hum
1028	66.5	5.5	328	3	AAy94744	Murine CD	1101	66	5.5	746	2	AAy29512	AAy29512 Human lun
1029	66.5	5.5	328	5	ABP28638	Streptoco	1102	66	5.5	746	3	AAE44461	AAE44461 Human lun
1030	66.5	5.5	328	5	ABP28639	Streptoco	1103	66	5.5	746	4	AAE13802	AAE13802 Human lun
1031	66.5	5.5	328	6	ABU46600	Protein e	1104	66	5.5	746	7	ADD66493	ADD66493 Human lun
1032	66.5	5.5	331	3	AAy94743	Murine CD	1105	66	5.5	746	7	ADSO87747	ADSO87747 Human lun
1033	66.5	5.5	347	4	AAE87443	Human gen	1106	66	5.5	775	7	ADG64508	ADG64508 Family B
1034	66.5	5.5	398	7	ABO63696	Klebsiell	1107	66	5.5	775	8	ADN59954	ADN59954 9ON therm
1035	66.5	5.5	426	6	ABP6582	Cow Ige h	1108	66	5.5	792	4	AAE09853	AAE09853 Novel hum
1036	66.5	5.5	429	3	AAE53587	Arabidops	1109	66	5.5	795	3	AAy95968	AAy95968 Human TAN
1037	66.5	5.5	433	3	AAE53586	Arabidops	1110	66	5.5	795	4	AAE68514	AAE68514 Human GTP
1038	66.5	5.5	439	4	AAE55609	Human pro	1111	66	5.5	795	4	AAE93162	AAE93162 Human pro
1039	66.5	5.5	451	2	AAy01520	Chicken C	1112	66	5.5	795	7	ADM43083	ADM43083 Human TAN
1040	66.5	5.5	459	7	ADG10496	Human STR	1113	66	5.5	800	4	AAW78334	AAW78334 Human pro
1041	66.5	5.5	514	7	ABO79462	Pseudomon	1114	66	5.5	800	7	ADF28095	ADF28095 Adiponec
1042	66.5	5.5	660	7	ABO83460	Pseudomon	1115	66	5.5	809	6	ADA20755	ADA20755 Soybean p
1043	66.5	5.5	725	2	AAy38831	Neisseria	1116	66	5.5	821	5	ABR43183	ABR43183 Human REM
1044	66.5	5.5	789	6	ABU33178	Protein e	1117	66	5.5	824	5	ABG92061	ABG92061 Human rem
1045	66.5	5.5	956	6	ABE82783	Human CYL	1118	66	5.5	827	4	AAE09855	AAE09855 Novel hum
1046	66.5	5.5	1008	7	ABO80673	Pseudomon	1119	66	5.5	844	6	ABR43200	ABR43200 Human REM
1047	66.5	5.5	2096	3	AAE41592	Human ORF	1120	66	5.5	855	3	AAy95969	AAy95969 Human TAN

1121	66	5.5	855	7	ADM43107	Agm43107 Human TAN	1194	65.5	5.4	643	6	ABU39109	Abu39109 Protein e
1122	66	5.5	863	7	ADC31681	Adc31681 Human nov	1195	65.5	5.4	681	6	ABO32529	Abc32529 Secreted
1123	66	5.5	877	4	AAE09850	Aae09850 Novel hum	1196	65.5	5.4	706	7	ADQ10138	Adq10138 Human pol
1124	66	5.5	908	4	AAE09839	Aae09839 Novel hum	1197	65.5	5.4	715	5	AAU00670	Aau00670 Pseudomon
1125	66	5.5	909	4	AAE09845	Aae09845 Novel hum	1198	65.5	5.4	715	5	ABO06670	Abu06670 Human TAN
1126	66	5.5	926	4	AAE09852	Aae09852 Novel hum	1199	65.5	5.4	715	5	ABB81000	Abb81000 Human neu
1127	66	5.5	944	6	ABB80172	Abb80172 A. fumiga	1200	65.5	5.4	715	5	ABO32527	Abc32527 Secreted
1128	66	5.5	953	7	ADC24816	Adc24816 Human bre	1201	65.5	5.4	715	8	ADQ10136	Adq10136 Human pol
1129	66	5.5	957	4	AAE09841	Aae09841 Novel hum	1202	65.5	5.4	847	4	ABG17337	Abg17337 Novel hum
1130	66	5.5	958	4	AAE09847	Aae09847 Novel hum	1203	65.5	5.4	932	5	ABG20666	Abg20666 Human tum
1131	66	5.5	961	4	AAE09854	Aae09854 Novel hum	1204	65.5	5.4	1101	6	ADJ70375	Adj70375 Breast ca
1132	66	5.5	992	4	AAE09843	Aae09843 Novel hum	1205	65.5	5.4	1101	7	ADJ70375	Adj70375 Human hea
1133	66	5.5	993	4	AAE09849	Aae09849 Novel hum	1206	65.5	5.4	1101	8	ADQ20338	Adq20338 Human sof
1134	66	5.5	1042	4	AAE09838	Aae09838 Novel hum	1207	65.5	5.4	1280	3	AAE48316	Aae48316 Arabidops
1135	66	5.5	1043	4	AAE09844	Aae09844 Novel hum	1208	65.5	5.4	1360	6	AAE32114	Aae32114 Human cyt
1136	66	5.5	1091	4	AAE09840	Aae09840 Novel hum	1209	65.5	5.4	1473	4	AAE21179	Aae21179 Human TRI
1137	66	5.5	1092	4	AAE09846	Aae09846 Novel hum	1210	65.5	5.4	1864	5	AAE21179	Aae21179 Human NAC
1138	66	5.5	1116	7	ABO75628	Abu75628 Pseudomon	1211	65.5	5.4	1864	6	ABU62065	Abu62065 Human mel
1139	66	5.5	1126	4	AAE09842	Aae09842 Novel hum	1212	65	5.4	109	4	AAU59034	Aau59034 Propionib
1140	66	5.5	1127	4	AAE09848	Aae09848 Novel hum	1213	65	5.4	109	6	ABM55553	Abm55553 Propionib
1141	66	5.5	1354	7	ADH88855	Adh88855 Human int	1214	65	5.4	122	4	AAU66966	Aau66966 Propionib
1142	66	5.5	1467	7	ADH88855	Adh88855 Enterococ	1215	65	5.4	122	6	ABM63485	Abm63485 Propionib
1143	66	5.5	1632	6	ABU21966	Abu21966 Protein e	1216	65	5.4	163	4	AAO5967	Aao5967 Phosphoin
1144	66	5.5	1641	4	ABG18356	Abg18356 Novel hum	1217	65	5.4	180	7	AAO23184	Aao23184 Dye-dideo
1145	66	5.5	1713	4	ABBS8422	Abbs8422 Drosophil	1218	65	5.4	137	8	ADN47561	Adn47561 Thermococ
1146	66	5.5	2012	4	ABG02199	Abg02199 Novel hum	1219	65	5.4	198	2	ABY74195	Aay74195 Human pro
1147	66	5.5	2089	2	AAW08333	Aaw08333 Cyclotell	1220	65	5.4	200	4	ABY69252	Abb69252 Drosophil
1148	66	5.5	2326	5	ABBS1068	Abbs1068 Rat NG2 p	1221	65	5.4	200	8	ADH42561	Adh42561 Novel hum
1149	66	5.5	2326	8	ADO31204	Ado31204 Rat NG2 p	1222	65	5.4	200	8	ADH42563	Adh42563 Novel hum
1150	65.5	5.4	136	3	AGS57787	Ag57787 Arabidops	1223	65	5.4	221	7	ADM04770	Adm04770 Human pro
1151	65.5	5.4	195	1	APR90731	Apr90731 Limulus p	1224	65	5.4	233	2	AAE22754	Aar22754 Reshaped
1152	65.5	5.4	202	5	ABP36316	Abp36316 Myo-inosi	1225	65	5.4	241	4	AAW24352	Aam24352 Human EST
1153	65.5	5.4	214	7	ADP04359	Adp04359 Bacterial	1226	65	5.4	249	4	ABB68402	Abb68402 Drosophil
1154	65.5	5.4	218	5	AAE19182	Aae19182 Human pro	1227	65	5.4	251	7	ADC39138	Adc39138 Novel hum
1155	65.5	5.4	234	5	ABG70052	Abg70052 Human pre	1228	65	5.4	251	8	ADH42565	Adh42565 Novel hum
1156	65.5	5.4	238	8	ADL93649	Adl93649 Human CD4	1229	65	5.4	264	8	ADN72615	Adn72615 Thale cre
1157	65.5	5.4	264	4	ABG01661	Abg01661 Novel hum	1230	65	5.4	279	7	ABM74023	Abm74023 DNA clone
1158	65.5	5.4	279	3	ABAI0683	Abai0683 C. glutam	1231	65	5.4	280	7	ADF76971	Adf76971 Novel hum
1159	65.5	5.4	279	3	ABAI0034	Abai0034 C. glutam	1232	65	5.4	306	7	ADE58981	Ad58981 Rat Prote
1160	65.5	5.4	279	3	ABAI0032	Abai0032 C. glutam	1233	65	5.4	306	7	ADE58989	Ad58989 Rat Prote
1161	65.5	5.4	279	4	ABAI79940	Abi79940 Corynebac	1234	65	5.4	306	7	ADE58993	Ad58993 Rat Prote
1162	65.5	5.4	279	4	ABG89878	Abg89878 C. glutami	1235	65	5.4	306	7	ADE58985	Ad58985 Rat Prote
1163	65.5	5.4	282	2	AAI37026	Aai37026 Chlamydia	1236	65	5.4	306	8	ADF42736	Adf42736 Rat FRP a
1164	65.5	5.4	353	4	AAU14730	Aau14730 Novel bon	1237	65	5.4	320	4	AAU03102	Aau03102 Thermococ
1165	65.5	5.4	372	4	ABBS8017	Abbs8017 Drosophil	1238	65	5.4	322	6	ADB09240	Abd09240 Alloiococ
1166	65.5	5.4	373	4	ABG35330	Abg35330 Novel hum	1239	65	5.4	324	4	ABB62686	Abb62686 Drosophil
1167	65.5	5.4	375	8	ADK13795	Adk13795 E. coli i	1240	65	5.4	348	4	AAW41060	Aam41060 Human pol
1168	65.5	5.4	375	2	AAW80937	Aaw80937 Human hea	1241	65	5.4	348	7	ADE09981	Ade09981 Novel pro
1169	65.5	5.4	379	7	ADE25555	Ade25555 Human LLP	1242	65	5.4	364	7	ABO66451	Abc66451 Klebssteli
1170	65.5	5.4	379	7	ADG14394	Adg14394 Human LLP	1243	65	5.4	406	5	ABG93295	Abg93295 C. albica
1171	65.5	5.4	382	2	AAW80940	Aaw80940 Human hea	1244	65	5.4	422	7	ADC39136	Adc39136 Novel hum
1172	65.5	5.4	382	7	ADG14398	Adg14398 Human LLP	1245	65	5.4	422	8	ADH42559	Adh42559 Novel hum
1173	65.5	5.4	389	6	ABM69987	Abm69987 Photorhab	1246	65	5.4	427	2	AAR32085	Aar32085 Benzene d
1174	65.5	5.4	401	5	ABY76399	Abb76399 Phaffia r	1247	65	5.4	430	4	AAU04136	Aau04136 Tomato RE
1175	65.5	5.4	421	6	ABO32530	Abc32530 Secreted	1248	65	5.4	445	7	ABO70247	Abu70247 Pseudomon
1176	65.5	5.4	421	8	ADQ10139	Adq10139 Human pol	1249	65	5.4	449	6	ABU08678	Abu08678 Novel hum
1177	65.5	5.4	427	6	ABP97603	Abp97603 Amino aci	1250	65	5.4	449	7	AAC38613	Aac38613 Human thy
1178	65.5	5.4	429	3	ABG28833	Abg28833 Arabidops	1251	65	5.4	449	7	ADC63370	Adc63370 Human nov
1179	65.5	5.4	433	3	AAE28832	Aae28832 Arabidops	1252	65	5.4	449	8	ADI40851	Adi40851 Human kin
1180	65.5	5.4	435	7	ADJ69123	Adj69123 Human hea	1253	65	5.4	449	8	ADN49356	Adn49356 Human kin
1181	65.5	5.4	442	3	AAE24513	Aae24513 Human hea	1254	65	5.4	449	8	ADP84606	Adp84606 Human bre
1182	65.5	5.4	450	8	ADN46391	Adn46391 Thermococ	1255	65	5.4	454	5	ABBO9145	Abb09145 Human pho
1183	65.5	5.4	454	7	ABO79970	Abu79970 Pseudomon	1256	65	5.4	454	7	ADG14228	Adg14228 Partial H
1184	65.5	5.4	487	4	AAU00628	Aau00628 Novel hum	1257	65	5.4	459	7	ADC51245	Adc51245 B. cepaci
1185	65.5	5.4	524	7	ADM04757	Adm04757 Human pro	1258	65	5.4	457	5	AAE25058	Aae25058 Human cal
1186	65.5	5.4	539	4	AAU00630	Aau00630 Novel hum	1259	65	5.4	470	7	ADE80781	Ade80781 Microsate
1187	65.5	5.4	539	7	ADN39981	Adn39981 Cancer/an	1260	65	5.4	471	7	ADE80782	Ade80782 Microsate
1188	65.5	5.4	575	7	ADB65022	Adb65022 Human pro	1261	65	5.4	501	7	ADE80780	Ade80780 Microsate
1189	65.5	5.4	586	4	AAU00629	Aau00629 Novel hum	1262	65	5.4	503	6	ABU31993	Abu31993 Protein e
1190	65.5	5.4	586	7	ADN39982	Adn39982 Cancer/an	1263	65	5.4	518	4	ABU47156	Abu47156 PCNA asso
1191	65.5	5.4	587	7	ADC96778	Adc96778 E. faeciu	1264	65	5.4	518	8	ADQ19220	Adq19220 Human sof
1192	65.5	5.4	625	4	ABG25129	Abg25129 Novel hum	1265	65	5.4	530	8	ADM87191	Adm87191 Human pro
1193	65.5	5.4	641	5	ADI28019	Adi28019 ECMCAD pr	1266	65	5.4	574	7	ABO66883	Abc66883 Klebssteli

1267	65	5.4	590	7	ADC73072	Adc73072 P chrysos	1340	65	5.4	1424	6	ABU03684	Abu03684 Human exp
1268	65	5.4	597	7	ADE28697	Ade28697 Human NOV	1341	65	5.4	1424	7	ADE76188	Ade76188 Human AIB
1269	65	5.4	597	8	ADM93442	Adm93442 Human NOV	1342	65	5.4	1434	7	AAR94380	Aar94380 Mouse pat
1270	65	5.4	608	7	ADD46676	Add46676 Rat Prote	1343	65	5.4	1434	2	AAW52199	Aaw52199 Mouse pat
1271	65	5.4	614	5	ABB91334	Abb91334 Herbicida	1344	65	5.4	1434	2	AAW72968	Aaw72968 Mouse pat
1272	65	5.4	622	5	AAR10795	Aar10795 Human pro	1345	65	5.4	1434	4	AAB67159	Aab67159 Murine pa
1273	65	5.4	622	5	ABJ05555	Abj05555 Breast ca	1346	65	5.4	1434	5	AAG79572	Aag79572 Mouse pat
1274	65	5.4	622	5	AU993354	Au993354 Human pro	1347	65	5.4	1434	7	ABU62271	Abu62271 Mouse pat
1275	65	5.4	622	5	AU993355	Au993355 Human pro	1348	65	5.4	1434	7	ADH62272	Adh62272 Mouse pat
1276	65	5.4	622	6	ABR47567	Abra47567 Breast ca	1349	65	5.4	1434	7	ADH62722	Adh62722 Mouse pat
1277	65	5.4	622	7	ADN39426	Adn39426 Cancer/an	1350	65	5.4	1434	8	ADA88980	Ade88980 Mouse pat
1278	65	5.4	622	7	ADN38794	Adn38794 Cancer/an	1351	65	5.4	1438	5	AAE19060	Aae19060 Human amp
1279	65	5.4	630	4	AAB934459	Aab934459 Human pro	1352	65	5.4	1447	2	AAR75375	Aar75375 Human pat
1280	65	5.4	630	7	AD80779	Ad80779 Microsate	1353	65	5.4	1447	2	AAW52200	Aaw52200 Human pat
1281	65	5.4	672	4	ABU52983	Abu52983 Human tes	1354	65	5.4	1447	2	AAW72969	Aaw72969 Human pat
1282	65	5.4	674	5	ABU05342	Abu05342 Pancreas-	1355	65	5.4	1447	4	AAE67163	Aae67163 Human pat
1283	65	5.4	674	5	ABU05347	Abu05347 Pancreas-	1356	65	5.4	1447	5	AAE19830	Aae19830 Human pat
1284	65	5.4	674	5	ABU05346	Abu05346 Pancreas-	1357	65	5.4	1447	5	AAE10931	Aae10931 Human pat
1285	65	5.4	674	6	AAE36063	Aae36063 Human tra	1358	65	5.4	1447	5	AAG79571	Aag79571 Human pat
1286	65	5.4	674	7	ADB85297	Adb85297 Human Na-	1359	65	5.4	1447	7	ABU62275	Abu62275 Human pat
1287	65	5.4	674	8	ADO09778	Ado09778 Human SGL	1360	65	5.4	1447	7	ADD46678	Add46678 Human pro
1288	65	5.4	681	5	AAO14202	Aao14202 Human tra	1361	65	5.4	1447	7	ADH62271	Adh62271 Human pat
1289	65	5.4	681	6	AAE36062	Aae36062 Human tra	1362	65	5.4	1447	7	ADH62731	Adh62731 Human pat
1290	65	5.4	681	8	ADJ81711	Adj81711 Human SMI	1363	65	5.4	1447	8	ADA88989	Ade88989 Human pat
1291	65	5.4	687	4	AAE05962	Aae05962 Human pho	1364	65	5.4	1522	2	AAE21975	Aae21975 Human ste
1292	65	5.4	700	7	ADJ70619	Adj70619 Human hea	1365	65	5.4	1447	7	ADH62275	Adh62275 Human pat
1293	65	5.4	710	4	AAE05957	Aae05957 Human pho	1366	65	5.4	1447	7	ADH62275	Adh62275 Human pat
1294	65	5.4	720	5	ABP89719	Abp89719 Human pol	1367	65	5.4	1447	7	ADH62271	Adh62271 Human pat
1295	65	5.4	724	3	AAE70451	Aae70451 Human mem	1368	65	5.4	1447	8	ADA88989	Ade88989 Human pat
1296	65	5.4	738	6	AAE36065	Aae36065 Human tra	1369	65	5.4	1522	2	AAE21975	Aae21975 Human ste
1297	65	5.4	745	6	AAE36064	Aae36064 Human tra	1370	65	5.4	5322	4	ABG18724	Abg18724 Novel hum
1298	65	5.4	777	3	AAE36070	Aae36070 Human can	1371	64.5	5.4	87	5	AAE25746	Aae25746 Rice Ft h
1299	65	5.4	848	5	ABB07494	Abb07494 Human lip	1372	64.5	5.4	108	3	AAE00624	Aae00624 Human sec
1300	65	5.4	849	5	ABB09144	Abb09144 Human pho	1373	64.5	5.4	109	8	ADG06823	Adg06823 Human E48
1301	65	5.4	849	7	ADE08121	Ade08121 Novel pro	1374	64.5	5.4	128	2	AAW06292	Aaw06292 Human squ
1302	65	5.4	849	7	ADG14226	Adg14226 Human PLA	1375	64.5	5.4	128	6	ABR48216	Abr48216 Human bla
1303	65	5.4	851	4	AAW78324	Aaw78324 Human pro	1376	64.5	5.4	128	7	ABW01524	Abw01524 Protein #
1304	65	5.4	877	5	AAE00938	Aae00938 M. prunae	1377	64.5	5.4	128	8	ADJ75520	Adj75520 Marker ge
1305	65	5.4	877	5	AAE22115	Aae22115 Metallosp	1378	64.5	5.4	128	8	ADN04230	Adn04230 Antipsori
1306	65	5.4	921	4	ABE50264	Abbe50264 DXF2p5860	1379	64.5	5.4	178	6	AAE092555	Aae092555 C glutami
1307	65	5.4	947	4	ABG20052	Abg20052 Novel hum	1380	64.5	5.4	202	5	ABG733613	Abg733613 Myo-inosi
1308	65	5.4	951	2	AAW81028	Aaw81028 ER intera	1381	64.5	5.4	206	5	ABG77308	Abg77308 Selected
1309	65	5.4	951	6	AAU03688	Aau03688 Human exp	1382	64.5	5.4	213	8	ADP44641	Adp44641 Human ant
1310	65	5.4	983	3	AAU70775	Aau70775 Follistat	1383	64.5	5.4	214	8	ADQ31272	Adq31272 Murine 11
1311	65	5.4	983	5	AAE22858	Aae22858 Human Zfs	1384	64.5	5.4	216	2	AAW70330	Aaw70330 Fibroblas
1312	65	5.4	983	6	ABU62108	Abu62108 Human fol	1385	64.5	5.4	227	8	ADP81208	Adp81208 Protein o
1313	65	5.4	987	4	ABG20044	Abg20044 Novel hum	1386	64.5	5.4	230	5	ABU11210	Abu11210 Yeast sel
1314	65	5.4	990	4	AAU27769	Aau27769 Human ful	1387	64.5	5.4	239	4	AAE48076	Aae48076 Human ext
1315	65	5.4	1117	4	AAE39633	Aae39633 Human pol	1388	64.5	5.4	253	6	ADL66900	Adl66900 Human ext
1316	65	5.4	1158	4	AAU29529	Aau29529 Novel hum	1389	64.5	5.4	253	6	ABU26748	Abu26748 Protein e
1317	65	5.4	1192	4	AAE39631	Aae39631 Human pol	1390	64.5	5.4	265	4	AAE81540	Aae81540 S. epider
1318	65	5.4	1225	4	AAE41419	Aae41419 Human pol	1391	64.5	5.4	278	7	ADM47287	Adm47287 Osteopont
1319	65	5.4	1225	4	AAE41418	Aae41418 Human pol	1392	64.5	5.4	280	5	AAU97607	Aau97607 Protein e
1320	65	5.4	1225	4	AAE41417	Aae41417 Human pol	1393	64.5	5.4	290	7	ADM47215	Adm47215 Osteopont
1321	65	5.4	1261	7	ADB82702	Adb82702 Human pro	1394	64.5	5.4	299	6	ABU27652	Abu27652 Protein e
1322	65	5.4	1291	3	AAE38592	Aae38592 Arabidops	1395	64.5	5.4	322	3	AAE32735	Aae32735 Eucalyptu
1323	65	5.4	1296	2	AAW47157	Aaw47157 Nevoid ba	1396	64.5	5.4	358	5	ABG62059	Abg62059 Human tum
1324	65	5.4	1343	8	ADM67208	Adm67208 Murine ad	1397	64.5	5.4	360	7	ABO72878	Abo72878 Pseudomon
1325	65	5.4	1371	3	AAE38591	Aae38591 Arabidops	1398	64.5	5.4	369	6	ADA33010	Ada33010 Acinetoba
1326	65	5.4	1412	4	AAE59278	Aae59278 Human SRC	1399	64.5	5.4	370	2	AAE60680	Aae60680 Murine tr
1327	65	5.4	1412	6	ABU03690	Abu03690 Human exp	1400	64.5	5.4	437	5	ABP40497	Abp40497 Staphyloc
1328	65	5.4	1412	6	ABU03685	Abu03685 Human exp	1401	64.5	5.4	455	4	AAU60912	Aau60912 Propionib
1329	65	5.4	1412	6	ABU03686	Abu03686 Human exp	1402	64.5	5.4	455	6	ABM57431	Abm57431 Propionib
1330	65	5.4	1412	7	ADJ70476	Adj70476 Human hea	1403	64.5	5.4	501	2	AAE49543	Aae49543 Human PRO
1331	65	5.4	1415	6	ABU03693	Abu03693 Human exp	1404	64.5	5.4	501	3	AAE51933	Aae51933 Human PRO
1332	65	5.4	1417	6	ABU03682	Abu03682 Human exp	1405	64.5	5.4	501	3	AAE51940	Aae51940 Human PRO
1333	65	5.4	1420	2	AAW81025	Aaw81025 AIB1 (Amp	1406	64.5	5.4	501	3	AAJ58631	Aaj58631 Human PRO
1334	65	5.4	1420	6	ABU03687	Abu03687 Human exp	1407	64.5	5.4	502	5	ABG62057	Abg62057 Human tum
1335	65	5.4	1420	6	ABU03683	Abu03683 Human exp	1408	64.5	5.4	508	7	ADB65334	Adb65334 Human pro
1336	65	5.4	1420	6	ABU03692	Abu03692 Human exp	1409	64.5	5.4	533	7	ABO60994	Abo60994 Klebsiell
1337	65	5.4	1424	6	ABU03694	Abu03694 Human exp	1410	64.5	5.4	534	4	AAE63674	Aae63674 Polypepti
1338	65	5.4	1424	6	ABU03681	Abu03681 Human exp	1411	64.5	5.4	550	2	AAE63674	Aae63674 Polypepti
1339	65	5.4	1424	6	ABU03681	Abu03681 Human exp	1412	64.5	5.4	550	2	AAE63674	Aae63674 Polypepti

1413	64.5	5.4	550	4	AAB73617	Mouse K10	Aab73617	Mouse K10	1486	64	5.3	288	6	ABU42835	Abu42835	Protein e
1414	64.5	5.4	560	5	ABB94304	Chlamydia	Abb94304	Chlamydia	1487	64	5.3	295	5	ABP39621	Abp39621	Staphyloc
1415	5.4	5.4	573	7	ADD30652	Plant yie	Add30652	Plant yie	1488	64	5.3	318	8	ADN46262	Adn46262	Thermococ
1416	64.5	5.4	573	8	ADI44321	Plant tra	Adi44321	Plant tra	1489	64	5.3	319	4	AAU03093	Aau03093	Thermococ
1417	64.5	5.4	605	4	AAB93421	Human pro	Aab93421	Human pro	1490	64	5.3	320	4	AAU03096	Aau03096	Thermococ
1418	64.5	5.4	609	2	AA36756	C. tracho	Aa36756	C. tracho	1491	64	5.3	320	4	AAU03095	Aau03095	Thermococ
1419	64.5	5.4	612	6	ABU37748	Protein e	Abu37748	Protein e	1492	64	5.3	320	4	AAU03101	Aau03101	Thermococ
1420	64.5	5.4	613	5	ABG93160	S. cerevi	Abg93160	S. cerevi	1493	64	5.3	320	4	AAU03100	Aau03100	Thermococ
1421	64.5	5.4	615	5	ABG62062	Human tum	Abg62062	Human tum	1494	64	5.3	320	4	AAU03099	Aau03099	Thermococ
1422	64.5	5.4	617	6	ABU15254	Protein e	Abu15254	Protein e	1495	64	5.3	320	4	AAU03094	Aau03094	Thermococ
1423	64.5	5.4	664	7	ADD69563	Pichia ja	Add69563	Pichia ja	1496	64	5.3	320	4	AAU03097	Aau03097	Thermococ
1424	64.5	5.4	707	2	AAR34131	Truncated	Aar34131	Truncated	1497	64	5.3	320	4	AAU03103	Aau03103	Thermococ
1425	64.5	5.4	779	6	ABM68355	Phototrab	Abm68355	Phototrab	1498	64	5.3	323	4	AAU03105	Aau03105	Thermococ
1426	64.5	5.4	812	2	AAR72797	Phospholi	Aar72797	Phospholi	1499	64	5.3	328	4	AAE04446	Aae04446	Murine Ho
1427	64.5	5.4	812	2	AAW06134	Phospholi	Aaw06134	Phospholi	1500	64	5.3	328	6	ABJ25476	Abj25476	Aspergill
1428	64.5	5.4	812	2	AAW25675	Phospholi	Aaw25675	Phospholi								
1429	64.5	5.4	830	5	ABB92549	Herbicida	Abb92549	Herbicida								
1430	64.5	5.4	834	7	ABO79399	Pseudomon	Abb79399	Pseudomon								
1431	64.5	5.4	1002	4	ABB61695	Drosophil	Abb61695	Drosophil								
1432	64.5	5.4	1002	4	ABB58811	Drosophil	Abb58811	Drosophil								
1433	64.5	5.4	1002	4	ABB5804	Drosophil	Abb5804	Drosophil								
1434	64.5	5.4	1002	4	ABB5834	Drosophil	Abb5834	Drosophil								
1435	64.5	5.4	1002	8	ADI30124	D. melano	Adi30124	D. melano								
1436	64.5	5.4	1002	8	ADI30124	D. melano	Adi30124	D. melano								
1437	64.5	5.4	1002	8	ADI30151	D. melano	Adi30151	D. melano								
1438	64.5	5.4	1002	8	ADI30152	D. melano	Adi30152	D. melano								
1439	64.5	5.4	1002	8	ADI30153	D. melano	Adi30153	D. melano								
1440	64.5	5.4	1014	2	AAW63673	Polypteti	Aaw63673	Polypteti								
1441	64.5	5.4	1014	4	AAB73616	Mouse K10	Aab73616	Mouse K10								
1442	64.5	5.4	1037	8	ADI30138	D. melano	Adi30138	D. melano								
1443	64.5	5.4	1041	8	ADI30137	D. melano	Adi30137	D. melano								
1444	64.5	5.4	1164	4	ABG30268	Novel hum	Abg30268	Novel hum								
1445	64.5	5.4	1172	6	ADA34784	Acinetoba	Ada34784	Acinetoba								
1446	64.5	5.4	1173	5	ABB93479	Herbicida	Abb93479	Herbicida								
1447	64.5	5.4	1220	3	AA378972	Rp1-WeB	Aay78972	Rp1-WeB								
1448	64.5	5.4	1227	7	AD671295	Novel hum	Ad671295	Novel hum								
1449	64.5	5.4	1260	4	ABBS9060	Drosophil	Abbs9060	Drosophil								
1450	64.5	5.4	1354	4	ABB69973	Drosophil	Abb69973	Drosophil								
1451	64.5	5.4	1815	5	ADH48726	NOV4B pro	Adh48726	NOV4B pro								
1452	64.5	5.4	1856	5	ADH48724	NOV4A pro	Adh48724	NOV4A pro								
1453	64.5	5.4	1889	8	ADM99797	Leptospir	Adm99797	Leptospir								
1454	64	5.3	180	7	AAO23181	Dye-dideo	Aao23181	Dye-dideo								
1455	64	5.3	180	7	AAO23175	Dye-dideo	Aao23175	Dye-dideo								
1456	64	5.3	180	7	AAO23185	Dye-dideo	Aao23185	Dye-dideo								
1457	64	5.3	180	7	AAO23183	Dye-dideo	Aao23183	Dye-dideo								
1458	64	5.3	180	7	AAO23176	Dye-dideo	Aao23176	Dye-dideo								
1459	64	5.3	180	7	AAO23178	Dye-dideo	Aao23178	Dye-dideo								
1460	64	5.3	180	7	AAO23182	Dye-dideo	Aao23182	Dye-dideo								
1461	64	5.3	180	7	AAO23187	Dye-dideo	Aao23187	Dye-dideo								
1462	64	5.3	180	7	AAO23174	Dye-dideo	Aao23174	Dye-dideo								
1463	64	5.3	180	7	AAO23179	Dye-dideo	Aao23179	Dye-dideo								
1464	64	5.3	212	5	ABP51955	Humanised	Abp51955	Humanised								
1465	64	5.3	214	2	AAW34504	Light cha	Aaw34504	Light cha								
1466	64	5.3	214	2	AAW34506	Light cha	Aaw34506	Light cha								
1467	64	5.3	214	2	AAW95615	Humanized	Aaw95615	Humanized								
1468	64	5.3	214	2	AAW30632	Recombina	Aaw30632	Recombina								
1469	64	5.3	214	2	AA308754	Human ant	Aay08754	Human ant								
1470	64	5.3	214	4	AAB66777	rhuMab CD	Aab66777	rhuMab CD								
1471	64	5.3	214	5	ABG31889	Humanised	Abg31889	Humanised								
1472	64	5.3	214	8	ADQ318342	Amino aci	Adk18342	Amino aci								
1473	64	5.3	214	8	ADQ31280	Humanised	Adq31280	Humanised								
1474	64	5.3	214	8	ADQ31278	Humanised	Adq31278	Humanised								
1475	64	5.3	216	2	AAW37915	Fibroblas	Aaw37915	Fibroblas								
1476	64	5.3	223	6	ABJ36940	Anti-CD40	Abj36940	Anti-CD40								
1477	64	5.3	236	4	AAU30086	Novel hum	Aau30086	Novel hum								
1478	64	5.3	237	2	AAW95622	PS1130 ex	Aaw95622	PS1130 ex								
1479	64	5.3	237	2	AAW30634	Recombina	Aaw30634	Recombina								
1480	64	5.3	237	4	ABG66784	Protein e	Abg66784	Protein e								
1481	64	5.3	237	5	ABG72187	Human zin	Abp72187	Human zin								
1482	64	5.3	237	6	ABP72745	Anti-CD18	Abp72745	Anti-CD18								
1483	64	5.3	247	5	ABG70338	Human MDD	Abg70338	Human MDD								
1484	64	5.3	264	4	ABG81596	S. epider	Ag81596	S. epider								
1485	64	5.3	286	8	ADH61292	INTSIG pr	Adh61292	INTSIG pr								

ALIGNMENTS

RESULT 1

AAB18923
ID AAB18923 standard; protein; 223 AA.

XX AAB18923;

DT 08-FEB-2001 (first entry)

DE A novel polypeptide designated PRO4408.

XX Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;
KW PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;
KW PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030;
KW PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;
KW insulinemia; kidney disorder; Bergers disease; nephropathy;
KW Schonlein-Henoch purpura; celiac disease; dermatitis herpetiformis;
KW Crohns disease.

OS Homo sapiens.

Key Location/Qualifiers

FT Peptide 1..22 "signal peptide"

FT Modified-site 54..60 /note= "N-myristoylation site"

FT Modified-site 59..68 /note= "tyrosine kinase phosphorylation site"

FT Modified-site 83..89 /note= "N-myristoylation site"

FT Modified-site 130..136 /note= "N-myristoylation site"

FT Modified-site 169..173 /note= "N-glycosylation site"

PN WO200056889-A2.

XX 28-SEP-2000.

XX 01-MAR-2000; 2000WO-US005601.

XX 23-MAR-1999; 99US-0125774P.

XX 23-MAR-1999; 99US-0125778P.

XX 24-MAR-1999; 99US-0125826P.

XX 31-MAR-1999; 99US-0127035P.

XX 05-APR-1999; 99US-0127706P.

XX 21-APR-1999; 99US-0130359P.

XX 27-APR-1999; 99US-0131270P.

XX 27-APR-1999; 99US-0131272P.

XX 04-MAY-1999; 99US-0132371P.

XX 04-MAY-1999; 99US-0132379P.

XX 25-MAY-1999; 99US-0132383P.

XX 25-MAY-1999; 99US-0135750P.

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PR 08-JUN-1999; 99US-0138166P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 09-DEC-1999; 99US-0170282P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Deenoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
XX Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2000-628263/60.
XX N-PSDB; AAA96350.
XX
XX Novel secreted and transmembrane polypeptides useful for diagnosing tumor
XX in a mammal, for identifying agonists and antagonists of the polypeptide
XX and for therapeutic use.
XX
XX Claim 12; Fig 30; 222pp; English.
XX
XX The present sequence represents a secreted or transmembrane polypeptide.
XX The specification describes polypeptides designated PRO1484, PRO4334,
XX PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,
XX PRO4356, PRO4352, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990,
XX PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is
XX useful for diagnosing tumour in a mammal. The polypeptides, their
XX agonists and antagonists are useful treating a condition associated with
XX expression or activity of the polypeptide. Conditions treated include
XX obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are
XX capable of inducing proliferation of mammalian kidney mesangial cells and
XX are therefore useful for treating kidney disorders associated with
XX decreased mesangial cell function such as Berger's disease or other
XX nephropathies associated with Schonlein-Henoch purpura, celiac disease,
XX dermatitis herpetiformis or Crohn's disease. The nucleic acids may be used
XX to generate transgenic animals for use in development and screening of
XX therapeutically useful reagents and also for chromosome identification
XX and tissue typing
XX
XX Sequence 223 AA;
XX
XX Query Match 100.0%; Score 1204; DB 3; Length 223;
XX Best Local Similarity 100.0%; Pred. No. 7.3e-128;
XX Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MGWTRLVTAALLGLMMVTVGDEDNENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
DB 1 MGWTRLVTAALLGLMMVTVGDEDNENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
QY 61 VPDCCNNYRQKITSMWEPVIVKFPAGVDGATYILNMVDPDAPSPRAEPQRQFRWHLWLTIDIG 120
DB 61 VPDCCNNYRQKITSMWEPVIVKFPAGVDGATYILNMVDPDAPSPRAEPQRQFRWHLWLTIDIG 120
QY 121 ADLKKGKIQOELSAYCAQSPPAHSGFHYQFFVYLQEGKVISILLPKENKTRGSWMKDRF 180
DB 121 ADLKKGKIQOELSAYCAQSPPAHSGFHYQFFVYLQEGKVISILLPKENKTRGSWMKDRF 180
QY 181 LNRPHLGEPEASTQFTQNTQDSFTLQAPRGRASEPKHKTRQ 223
DB 181 LNRPHLGEPEASTQFTQNTQDSFTLQAPRGRASEPKHKTRQ 223
XX
RESULT 2
AAU83707
ID AAU83707 standard; protein; 223 AA.
XX
XX AAU83707;
XX
XX 08-MAY-2002 (first entry)
XX
XX Human PRO protein, Seq ID No 232.
XX
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
XX breast cancer; prostate tumour; rectal tumour; liver tumour;
XX pericyte cell proliferation; chondrocyte cell proliferation;
```

```
KW tumour necrosis factor-alpha.
XX
XX Homo sapiens.
XX
XX WO200208288-A2.
XX
XX 31-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-US021066.
XX
XX 20-JUL-2000; 2000US-0219556P.
XX 25-JUL-2000; 2000US-0220585P.
XX 25-JUL-2000; 2000US-0220605P.
XX 25-JUL-2000; 2000US-0220607P.
XX 25-JUL-2000; 2000US-0220624P.
XX 25-JUL-2000; 2000US-0220638P.
XX 25-JUL-2000; 2000US-0220666P.
XX 25-JUL-2000; 2000US-0220666P.
XX 26-JUL-2000; 2000US-0220893P.
XX 26-JUL-2000; 2000WO-US020710.
XX 01-AUG-2000; 2000US-0222425P.
XX 23-AUG-2000; 2000US-0227133P.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023328.
XX 10-NOV-2000; 2000WO-US030873.
XX 28-NOV-2000; 2000US-0253646P.
XX 01-DEC-2000; 2000WO-US032678.
XX 20-DEC-2000; 2000US-00747259.
XX 20-DEC-2000; 2000WO-US034956.
XX 28-FEB-2001; 2001WO-US006520.
XX 01-MAR-2001; 2001WO-US006666.
XX 22-MAR-2001; 2001US-00816744.
XX 10-MAY-2001; 2001US-00854208.
XX 10-MAY-2001; 2001US-00854280.
XX 25-MAY-2001; 2001WO-US017092.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
XX WPI; 2002-172001/22.
XX N-PSDB; ABK33651.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful for treating a PRO related disorder and for diagnosing tumors such
XX as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
XX or liver tumor.
XX
XX Claim 11; Fig 232; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX agonists and antagonists are useful for treating a PRO related disorder.
XX The PRO polypeptides are useful for diagnosing tumours, especially lung
XX cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
XX liver tumour. The PRO polypeptides are useful for stimulating the
XX proliferation of, or gene expression, in pericyte cells, for stimulating
XX the proliferation or differentiation of chondrocyte cells, for
XX stimulating the release of tumour necrosis factor-alpha from human blood,
XX for stimulating or inhibiting the proliferation of normal human dermal
XX fibroblast cells. The PRO polypeptide may also be used as molecular
XX weight markers and for tissue typing. The PRO nucleic acids have
XX applications in molecular biology, including use as hybridisation probes,
XX and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
XX protein sequences of the invention
XX
XX Sequence 223 AA;
XX
XX Query Match 100.0%; Score 1204; DB 5; Length 223;
XX Best Local Similarity 100.0%; Pred. No. 7.3e-128;
XX Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MGWTRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
DB 1 MGWTRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
QY 61 VPDCCNNYRQKITSWMPEIVKFPFGAVDGTATYILVMVDPDAPSPRAEPFRQRFWRHMLVTDIKG 120
DB 61 VPDCCNNYRQKITSWMPEIVKFPFGAVDGTATYILVMVDPDAPSPRAEPFRQRFWRHMLVTDIKG 120
QY 121 ADLKKGKIQQOELSAYQAPSPPAHSGFHRHYOFFVYLQEGKVISLLPKENKTRGSKWMDRF 180
DB 121 ADLKKGKIQQOELSAYQAPSPPAHSGFHRHYOFFVYLQEGKVISLLPKENKTRGSKWMDRF 180
QY 181 LNRPHLGEPEASTQFMTQNTQYQDSPTLQAPRGRASEPKHKTRQ 223
DB 181 LNRPHLGEPEASTQFMTQNTQYQDSPTLQAPRGRASEPKHKTRQ 223

RESULT 3
ABB84969
ID ABB84969 standard; protein; 223 AA.
XX AC ABB84969;
XX DT 16-MAY-2002 (first entry)
XX DE Human PR04408 protein sequence SEQ ID NO:306.
XX KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
XX KW vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
XX KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
XX KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
XX KW age-related macular degeneration; arterial restenosis; angina;
XX KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
XX KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
XX KW wound healing; chromosome mapping; gene mapping.
XX OS Homo sapiens.
XX PN WO200200690-A2.
XX PD 03-JAN-2002.
XX PF 20-JUN-2001; 2001WO-US019692.
XX PR 23-JUN-2000; 2000US-0213637P.
XX PR 20-JUL-2000; 2000US-0219556P.
XX PR 25-JUL-2000; 2000US-0220624P.
XX PR 25-JUL-2000; 2000US-0220684P.
XX PR 28-JUL-2000; 2000WO-US020710.
XX PR 02-AUG-2000; 2000US-0222695P.
XX PR 17-AUG-2000; 2000US-00643657.
XX PR 23-AUG-2000; 2000WO-US023522.
XX PR 24-AUG-2000; 2000WO-US023328.
XX PR 07-SEP-2000; 2000US-0230978P.
XX PR 18-SEP-2000; 2000US-00664610.
XX PR 18-SEP-2000; 2000US-00665350.
XX PR 24-OCT-2000; 2000US-0242922P.
XX PR 08-NOV-2000; 2000US-00709238.
XX PR 08-NOV-2000; 2000WO-US030952.
XX PR 10-NOV-2000; 2000WO-US030873.
XX PR 01-DEC-2000; 2000WO-US032678.
XX PR 20-DEC-2000; 2000US-00747259.
XX PR 22-JAN-2001; 2000WO-US034956.
XX PR 28-FEB-2001; 2001US-00796498.
XX PR 28-FEB-2001; 2001WO-US006520.
XX PR 01-MAR-2001; 2001WO-US006666.
XX PR 09-MAR-2001; 2001US-00802706.
XX PR 14-MAR-2001; 2001US-00808689.
XX PR 25-MAR-2001; 2001US-00816744.
XX PR 05-APR-2001; 2001US-00828366.
XX PR 10-MAY-2001; 2001US-00854208.
```

```
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 30-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
XX (GETH ) GENENTECH INC.
XX PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
XX PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
XX PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX DR WPI; 2002-090516/12.
XX DR N-PSDB; ABL88224.
XX PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX PT infarction), endothelial or angiogenic disorders in a mammal.
XX PS Claim 11; Fig 306; 565pp; English.
XX CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
XX CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
XX CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
XX CC activities, and can be used in gene therapy. The PRO polynucleotides,
XX CC proteins, agonists and antagonists are useful for treating or diagnosing
XX CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
XX CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
XX CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
XX CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
XX CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
XX CC healing. The PRO polynucleotides have applications in molecular biology,
XX CC including use as hybridisation probes, and in chromosome and gene
XX CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
XX CC exemplification of the present invention
XX SQ Sequence 223 AA;
XX Query Match 100.0%; Score 1204; DB 5; Length 223;
XX Best Local Similarity 100.0%; Pred. No. 7.3e-128;
XX Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGWTRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
DB 1 MGWTRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
QY 61 VPDCCNNYRQKITSWMPEIVKFPFGAVDGTATYILVMVDPDAPSPRAEPFRQRFWRHMLVTDIKG 120
DB 61 VPDCCNNYRQKITSWMPEIVKFPFGAVDGTATYILVMVDPDAPSPRAEPFRQRFWRHMLVTDIKG 120
QY 121 ADLKKGKIQQOELSAYQAPSPPAHSGFHRHYOFFVYLQEGKVISLLPKENKTRGSKWMDRF 180
DB 121 ADLKKGKIQQOELSAYQAPSPPAHSGFHRHYOFFVYLQEGKVISLLPKENKTRGSKWMDRF 180
QY 181 LNRPHLGEPEASTQFMTQNTQYQDSPTLQAPRGRASEPKHKTRQ 223
DB 181 LNRPHLGEPEASTQFMTQNTQYQDSPTLQAPRGRASEPKHKTRQ 223

RESULT 4
ABB95575
ID ABB95575 standard; protein; 223 AA.
XX AC ABB95575;
XX DT 19-JUL-2002 (first entry)
XX DE Human angiogenesis related protein PR04408 SEQ ID NO: 306.
XX KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
XX KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
```


KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnery;

KW antiarteriosclerotic.

OS Homo sapiens.

XX WO200208284-A2.

XX 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US021735.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220624P.

XX 25-JUL-2000; 2000US-0220664P.

XX 28-JUL-2000; 2000WO-US020710.

XX 02-AUG-2000; 2000US-0222695P.

XX 17-AUG-2000; 2000US-00643657.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

XX 07-SEP-2000; 2000US-0230978P.

XX 18-SEP-2000; 2000US-00664610.

XX 18-SEP-2000; 2000US-00665350.

XX 24-OCT-2000; 2000US-0242922P.

XX 08-NOV-2000; 2000US-00709238.

XX 08-NOV-2000; 2000WO-US030952.

XX 10-NOV-2000; 2000WO-US030873.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000US-00747259.

XX 20-DEC-2000; 2000WO-US034956.

XX 23-JAN-2001; 2001US-00767609.

XX 28-FEB-2001; 2001US-00796498.

XX 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2001; 2001WO-US006666.

XX 09-MAR-2001; 2001US-00802706.

XX 14-MAR-2001; 2001US-00808689.

XX 22-MAR-2001; 2001US-00816744.

XX 05-APR-2001; 2001US-00828366.

XX 10-MAY-2001; 2001US-00854208.

XX 10-MAY-2001; 2001US-00854280.

XX 25-MAY-2001; 2001US-00866028.

XX 25-MAY-2001; 2001US-00866034.

XX 30-MAY-2001; 2001WO-US017092.

XX 30-MAY-2001; 2001US-00870574.

XX 01-JUN-2001; 2001WO-US017443.

XX 20-JUN-2001; 2001WO-US019692.

XX (GETH) GENENTECH INC.

XX (BAKE/) BAKER K P.

XX (FERE/) FERRARA N.

XX (GERB/) GERBER H.

XX (GERE/) GERRITSEN M E.

XX (GODD/) GODDARD A.

XX (GODO/) GODOWSKI P J.

XX (GURN/) GURNEY A L.

XX (HILL/) HILLAN K J.

XX (MARS/) MARSTERS S A.

XX (PANJ/) PAN J.

XX (PAON/) PAONI N F.

XX (STEP/) STEPHAN J F.

XX (WATA/) WATANABE C K.

XX (WILL/) WILLIAMS P M.

XX (WOOD/) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

XX Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI; 2002-171999/22.

XX N-PSDB; ABL95713.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial

PT infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 306; 567pp; English.

XX The present invention provides the protein and coding sequences of human

CC PRO proteins. These are useful for treating or diagnosing a

CC cardiovascular, endothelial or angiogenic disorder, including cardiac

CC hypertrophy, trauma, cancer, age-related macular degeneration,

CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,

CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour

CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound

CC healing. The present sequence is a PRO protein of the invention

XX

SQ Sequence 223 AA;

Query Match 100.0%; Score 1204; DB 5; Length 223;

Best Local Similarity 100.0%; Pred. No. 7.3e-128;

Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGMTMLVTAALLGLMMVVTGDENSPCAHEALDEDTLFCQGLEVFYFPELGNIGCKV 60

Db 1 MGMTMLVTAALLGLMMVVTGDENSPCAHEALDEDTLFCQGLEVFYFPELGNIGCKV 60

QY 61 VPDNNYRQKITSWMEPIVKFPGAVDGYILVMVDPDAPSPRAEPRQRFWRHMLVTDIKG 120

Db 61 VPDNNYRQKITSWMEPIVKFPGAVDGYILVMVDPDAPSPRAEPRQRFWRHMLVTDIKG 120

QY 121 ADLKKGKIQOELSAYQAPSPAHSGFHYQFVYLOEGKVLSLLPENKTRGSKWMDRF 180

Db 121 ADLKKGKIQOELSAYQAPSPAHSGFHYQFVYLOEGKVLSLLPENKTRGSKWMDRF 180

QY 181 LNRFLHGEPEASTQFTQNTQYQDSPTLQAPGRASEPKHKTRQR 223

Db 181 LNRFLHGEPEASTQFTQNTQYQDSPTLQAPGRASEPKHKTRQR 223

RESULT 5

ABU69117

ID ABU69117 standard; protein; 223 AA.

XX AC ABU69117;

XX DT 02-JUN-2003 (first entry)

XX DE Human PRO polypeptide #15.

XX KW Human; secreted and transmembrane protein; bone disorder; obesity;

KW cartilage disorder; sports injury; arthritis; diabetes mellitus;

KW hypo-insulinaemia; obesity; hyper-insulinaemia; thalassaemia;

KW haemoglobin-associated disorder; kidney disorder; Berger disease;

KW mesangial cell function; nephropathy; Schonlein-Henoch purpura;

KW celiac disease; dermatitis herpetiformis; Crohn's disease; anorectic;

KW antiarthritic; antidiabetic; antianaemic; nephrotropic; antiinflammatory.

XX OS Homo sapiens.

XX XN US2003032061-A1.

XX PD 13-FEB-2003.

XX PF 26-DEC-2001; 2001US-00036214.

XX PR 15-MAY-1998; 98US-0085579P.

XX PR 15-DEC-1998; 98US-0112514P.

XX PR 22-DEC-1998; 98US-0113300P.

XX PR 23-DEC-1998; 98US-0113430P.

XX PR 23-DEC-1998; 98US-0113605P.

XX PR 23-DEC-1998; 98US-0113621P.

XX PR 23-DEC-1998; 98US-0114140P.

XX PR 12-JAN-1999; 99US-0115552P.

XX PR 22-JAN-1999; 99US-0116843P.

XX PR 23-MAR-1999; 99US-0125774P.

XX PR 23-MAR-1999; 99US-0125778P.

24-MAR-1999; 99US-0125826P.
 31-MAR-1999; 99US-0127035P.
 05-APR-1999; 99US-0127706P.
 13-APR-1999; 99US-0129122P.
 21-APR-1999; 99US-0130359P.
 27-APR-1999; 99US-0131270P.
 27-APR-1999; 99US-0131272P.
 27-APR-1999; 99US-0131291P.
 04-MAY-1999; 99US-0132371P.
 04-MAY-1999; 99US-0132379P.
 04-MAY-1999; 99US-0132383P.
 14-MAY-1999; 99WO-US010733.
 25-MAY-1999; 99US-0135750P.
 08-JUN-1999; 99US-0138156P.
 20-JUL-1999; 99US-0144791P.
 03-AUG-1999; 99US-0146970P.
 29-OCT-1999; 99US-0162506P.
 02-DEC-1999; 99WO-US028551.
 22-DEC-1999; 99WO-US030720.
 01-MAR-2000; 2000WO-US005601.
 02-MAR-2000; 2000WO-US005841.
 22-MAY-2000; 2000WO-US014042.
 02-JUN-2000; 2000WO-US015264.
 23-AUG-2000; 2000WO-US023522.
 24-AUG-2000; 2000WO-US023328.
 01-DEC-2000; 2000WO-US032678.
 20-DEC-2000; 2000WO-US034956.
 28-FEB-2001; 2001WO-US006520.
 01-JUN-2001; 2001WO-US017800.
 20-JUN-2001; 2001WO-US019692.
 29-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.
 16-AUG-2001; 2001US-00931836.
 (GETH) GENENTECH INC.
 Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
 Stewart TA, Watanabe CK, Wood WI, Zhang Z;
 WPI; 2003-341962/32.
 N-PSDB; ACA06170.
 Novel isolated PRO polypeptides e.g., PRO4334, PRO1122, PRO1889, PRO1890,
 PRO1887, PRO1785, PRO4353, useful for treating sports injuries,
 arthritis, diabetes, obesity, hyper- or hypo-insulinemia.
 Claim 12; Fig 30; 194pp; English.
 The present invention relates to the isolation of novel human PRO
 polypeptides, and the polynucleotide sequences encoding them. The PRO
 polypeptides and polynucleotides are useful in diagnosing or treating
 various bone and/or cartilage disorders (e.g. sports injuries,
 arthritis), various insulin deficient states (e.g. diabetes mellitus,
 hypo-insulinaemia), obesity, hyper-insulinaemia, haemoglobin-associated
 disorders (e.g. thalassaemia), kidney disorders associated with
 decreased mesangial cell function (e.g. Berger disease), or other
 nephropathies associated with Schönlain-Henoch purpura, celiac disease,
 dermatitis herpetiformis or Crohn's disease. The PRO polynucleotide
 sequences may be used as hybridisation probes in chromosome and gene
 mapping, or in generating antisense RNA and DNA. They are also useful in
 preparing PRO polypeptides, in assays to identify other proteins or
 molecules involved in binding reaction, to generate transgenic animals or
 knockout animals, which in turn are useful in the development and
 screening of therapeutically useful reagents, for chromosome
 identification, and tissue typing. The PRO polypeptides and nucleic acid
 molecules are also useful in gene therapy, and as molecular weight
 markers for protein electrophoresis purposes. Anti-PRO antibodies may be
 used in diagnostic assays for PRO polypeptides, or for the affinity
 purification of the polypeptides from recombinant cell culture or natural
 sources. ABU69103-ABU69125 represent the human PRO polypeptides of the
 invention

SQ Sequence 223 AA;
 Query Match 100.0%; Score 1204; DB 6; Length 223;
 Best Local Similarity 100.0%; Pred. No. 7.3e-128;
 Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGWTRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
 DB 1 MGWTRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
 QY 61 VPDNNYRQKITSWMPEIVKFGAVDGTATYLVWVDPDAPSPRAEPRORFWRHMLVTDIKG 120
 DB 61 VPDNNYRQKITSWMPEIVKFGAVDGTATYLVWVDPDAPSPRAEPRORFWRHMLVTDIKG 120
 QY 121 ADLKKGKIQQEQLSAYQAPSPHSGFHRFYQFFVYLQEGKVISLLPKENKTRGSKMDRF 180
 DB 121 ADLKKGKIQQEQLSAYQAPSPHSGFHRFYQFFVYLQEGKVISLLPKENKTRGSKMDRF 180
 QY 181 LNRPHLGEPEASTQFTQNTQYQDSPTTLOAPRGRASEPKHKTRQ 223
 DB 181 LNRPHLGEPEASTQFTQNTQYQDSPTTLOAPRGRASEPKHKTRQ 223
 RESULT 6
 ABU0854
 ID ABU0854 standard; protein; 223 AA.
 XX
 AC ABU0854;
 XX
 DT 23-JUN-2003 (first entry)
 XX
 DE Human PRO polypeptide #116.
 XX
 KW Human; PRO polypeptide; secreted and transmembrane protein;
 anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN US2003036635-A1.
 XX
 PD 20-FEB-2003.
 XX
 PF 28-AUG-2002; 2002US-00230163.
 XX
 PR 25-JUL-2000; 2000US-0220638P.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 XX (GETH) GENENTECH INC.
 PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-342045/32.
 DR N-PSDB; ACA66956.
 XX
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for the manufacture of a medicament for diagnosing or treating
 PT tumor.
 XX
 PS Claim 11; Fig 232; 314pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides and polynucleotides are useful for preparing a medicament
 CC useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
 CC useful in diagnostic assays for PRO, by detecting its expression in
 CC specific cells, tissues or serum, and for affinity purification of PRO
 CC from recombinant cell culture or natural sources. ABU80739-ABU80860
 CC represent the human PRO polypeptides of the invention. Note: The sequence
 CC data for this patent was obtained in electronic format directly from the

```
CC USPTO web site at seqdata.uspto.gov/psipsdidentry.html
XX Sequence 223 AA;
SQ

Query Match 100.0%; Score 1204; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.3e-128;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGMTMLVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
Db 1 MGMTMLVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60

Qy 61 VPCNNYRQKITSWMPEIVKFPFGAVDGTATYILVMVDPDAPRAEPQRFWRHVLVTDIKG 120
Db 61 VPCNNYRQKITSWMPEIVKFPFGAVDGTATYILVMVDPDAPRAEPQRFWRHVLVTDIKG 120

Qy 121 ADLKKGIQOELSAYQAPSPPAHSGFHRYPFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
Db 121 ADLKKGIQOELSAYQAPSPPAHSGFHRYPFFVYLOEGKVISLLPKENKTRGSKWMDRF 180

Qy 181 LNRPHLGEPEASTQFMNTQNYQDSPTLQAPRGRASEPKHKTRQ 223
Db 181 LNRPHLGEPEASTQFMNTQNYQDSPTLQAPRGRASEPKHKTRQ 223

RESULT 7
ABO33820
ID ABO33820 standard; protein; 223 AA.
XX
AC ABO33820;
XX
DT 17-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO4408.
XX
KW Human; secreted and transmembrane protein; PRO; cytosolic;
KW antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; bone disorder; cartilage disorder; sports injury;
KW arthritis; wound.
XX
OS Homo sapiens.
XX
XX US2003045687-A1.
XX
PD 06-MAR-2003.
XX
PF 12-AUG-2002; 2002US-00218631.
XX
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH ) GENENTECH INC.
XX
FI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2003-512315/48.
DR N-PSDB; ACD68708.
XX
XX New genes, and its encoded secreted and transmembrane polypeptides,
XX useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
XX pericyte proliferation, especially for treating lung tumors, arthritis or
XX wounds in a mammal.
XX
PS Claim 11; Fig 232; 314pp; English.
XX
CC The invention describes an isolated nucleic acid molecule comprising a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
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PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005641.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 16-AUG-2001; 2001US-00931836.
XX (GETH) GENENTECH INC.
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-341326/32.
DR N-PSDB; ACA06113.
XX New PRO polypeptides and nucleic acid molecules, useful for diagnosing or
PT treating diabetes mellitus, cancers, septic shock, inflammatory bowel
PT disease or asthma, or in gene therapy, chromosome identification or
PT tissue typing.
XX Claim 12; Fig 30; 196pp; English.
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful in diagnosing or treating non
CC -insulin dependent diabetes mellitus, cancers, septic shock, rheumatoid
CC arthritis, graft-versus-host disease, stroke, cardiac ischaemia,
CC psoriasis, inflammatory bowel disease or asthma. The PRO polynucleotide
CC sequences may be used as hybridisation probes in chromosome and gene
CC mapping, or in generating antisense RNA and DNA. They are also useful in
CC preparing PRO polypeptides, in assays to identify other proteins or
CC molecules involved in binding reaction, to generate transgenic animals or
CC knockout animals, which in turn are useful in the development and
CC screening of therapeutically useful reagents, for chromosome
CC identification, and tissue typing. The PRO polypeptides and nucleic acid
CC molecules are also useful in gene therapy, and as molecular weight
CC markers for protein electrophoresis purposes. Anti-PRO antibodies may be
CC used in diagnostic assays for PRO polypeptides, or for the affinity
CC purification of the polypeptides from recombinant cell culture or natural
CC sources. ABU69080-ABU69102 represent the human PRO polypeptides of the
CC invention
XX SQ Sequence 223 AA;
Query Match 100.0%; Score 1204; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.3e-128;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGWTRLVTAALLGLMMVVTGDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
DB 1 MGWTRLVTAALLGLMMVVTGDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
QY 61 VPDCNNYRQKITSWMEPIVKFPGAVDGTATLVNVPDAPSPRAEPQRFWRHVLVTDIKG 120
DB 61 VPDCNNYRQKITSWMEPIVKFPGAVDGTATLVNVPDAPSPRAEPQRFWRHVLVTDIKG 120
QY 121 ADLKKGIQGEISAYQAPSPPAHSGFHYQFFVYLOEGKVISILLPKENKTRGSKMDRF 180
DB 121 ADLKKGIQGEISAYQAPSPPAHSGFHYQFFVYLOEGKVISILLPKENKTRGSKMDRF 180
QY 181 LNRFHLEPEASTQFMTQNTQYQDSPTLQAPGRASEPKHKTQR 223
DB 181 LNRFHLEPEASTQFMTQNTQYQDSPTLQAPGRASEPKHKTQR 223

RESULT 10

ABU82163
ID ABU82163 standard; protein; 223 AA.

XX AC ABU82163;

XX DT 25-JUN-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO4408.

XX Human; secreted and transmembrane protein; PRO; cardiac; cytostatic;
KW antiangiogenic; hypotensive; vulnery; antiarteriosclerotic;
KW gene therapy; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; cardiac hypertrophy; trauma; cancer;
KW age-related macular degeneration; atherosclerosis; hypertension;
KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
KW liver carcinoma; wound healing; chromosome mapping; gene mapping.

XX OS Homo sapiens.

XX PN US2003088063-A1.

XX PD 08-MAY-2003.

XX PF 12-AUG-2002; 2002US-00219003.

XX PR 25-JUL-2000; 2000US-0220664P.

XX PR 01-JUN-2001; 2001WO-US017800.

XX PR 29-JUN-2001; 2001WO-US021066.

XX PR 09-APR-2002; 2002US-00119480.

XX PA (GETH) GENENTECH INC.

XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX DR WPI; 2003-393229/37.
DR N-PSDB; ACA68612.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.

XX PS Claim 11; Fig 232; 314pp; English.

XX The invention describes one hundred and eighty seven nucleic acids
CC encoding novel human secreted and transmembrane (PRO) polypeptides. The
CC PRO nucleic acids, polypeptides, agonists and antagonists are useful for
CC treating or diagnosing a cardiovascular, endothelial or angiogenic
CC disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
CC related macular degeneration, atherosclerosis, hypertension, arterial
CC restenosis, rheumatoid arthritis, angina, myocardial infarctions,
CC thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
CC carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
CC have applications in molecular biology, including use as hybridisation
CC probes, and in chromosome and gene mapping. This is the amino acid
CC sequence of a novel human secreted and transmembrane PRO polypeptide
XX SQ Sequence 223 AA;

Query Match 100.0%; Score 1204; DB 6; Length 223;

Best Local Similarity 100.0%; Pred. No. 7.3e-128;

Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWTRLVTAALLGLMMVVTGDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60

DB 1 MGWTRLVTAALLGLMMVVTGDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60

QY 61 VPDCNNYRQKITSWMEPIVKFPGAVDGTATLVNVPDAPSPRAEPQRFWRHVLVTDIKG 120

DB 61 VPDCNNYRQKITSWMEPIVKFPGAVDGTATLVNVPDAPSPRAEPQRFWRHVLVTDIKG 120

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Qy 121 ADLKGKIQGQELSAQAPSPPAHSGFHRVYQFFVYLQEGKVISLLPKENKTRGSWKMDRF 180
Db 121 ADLKGKIQGQELSAQAPSPPAHSGFHRVYQFFVYLQEGKVISLLPKENKTRGSWKMDRF 180
Qy 181 LNRFHGLGEPEASTQFTMTQNTQDSPTLQAPRGRASEPKHKTRQR 223
Db 181 LNRFHGLGEPEASTQFTMTQNTQDSPTLQAPRGRASEPKHKTRQR 223

RESULT 11
ABU81558
ID ABU81558 standard; protein; 223 AA.
XX
AC ABU81558;
XX
DT 24-JUN-2003 (first entry)
XX
DE Human secreted polypeptide PRO4408.
XX
KW Human; inflammatory disease; organ failure; atherosclerosis; cancer;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW differentiation disorder; cell adhesion disorder; skin disorder;
KW neural receptor disorder; diabetic complication; tissue typing.
XX
OS Homo sapiens.
XX
XX US2002192751-A1.
XX
PN 19-DEC-2002.
XX
PF 26-DEC-2001; 2001US-00036041.
XX
PR 15-MAY-1998; 98US-0085579P.
PR 15-DEC-1998; 98US-0112514P.
PR 22-DEC-1998; 98US-0113300P.
PR 23-DEC-1998; 98US-0113430P.
PR 23-DEC-1998; 98US-0113605P.
PR 23-DEC-1998; 98US-0113621P.
PR 23-DEC-1998; 98US-0114140P.
PR 12-JAN-1999; 98US-0115552P.
PR 23-JAN-1999; 98US-0116843P.
PR 23-MAR-1999; 98US-0125774P.
PR 23-MAR-1999; 98US-0125778P.
PR 24-MAR-1999; 98US-0125826P.
PR 31-MAR-1999; 98US-0127035P.
PR 05-APR-1999; 98US-0127706P.
PR 13-APR-1999; 98US-0129122P.
PR 21-APR-1999; 98US-0130359P.
PR 27-APR-1999; 98US-0131270P.
PR 27-APR-1999; 98US-0131272P.
PR 27-APR-1999; 98US-0131291P.
PR 04-MAY-1999; 98US-0132371P.
PR 04-MAY-1999; 98US-0132379P.
PR 04-MAY-1999; 98US-0132383P.
PR 14-MAY-1999; 98US-0132383P.
PR 25-MAY-1999; 98US-0132383P.
PR 08-JUN-1999; 98US-0135750P.
PR 08-JUN-1999; 98US-0138166P.
PR 20-JUL-1999; 98US-0144791P.
PR 03-AUG-1999; 98US-0146970P.
PR 29-OCT-1999; 98US-0162506P.
PR 02-DEC-1999; 98US-0162506P.
PR 02-DEC-1999; 98US-0162506P.
PR 02-DEC-1999; 98US-0162506P.
PR 01-MAR-2000; 98US-0162506P.
PR 02-MAR-2000; 98US-0162506P.
PR 22-MAY-2000; 98US-0162506P.
PR 02-JUN-2000; 98US-0162506P.
PR 23-AUG-2000; 98US-0162506P.
PR 24-AUG-2000; 98US-0162506P.
PR 01-DEC-2000; 98US-0162506P.
PR 20-DEC-2000; 98US-0162506P.
PR 28-FEB-2001; 98US-0162506P.
PR 01-JUN-2001; 98US-0162506P.
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PR 20-JUN-2001; 2001US-00036041.
PR 20-JUN-2001; 2001US-00036041.
PR 09-JUL-2001; 2001US-00036041.
PR 16-AUG-2001; 2001US-00036041.
XX
PA (GETH ) GENENTECH INC.
XX
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-341079/32.
DR N-PSDB; ACA67736.
XX
XX New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.
XX
PS Claim 12; Fig 30; 195pp; English.
XX
CC The invention relates to an isolated nucleic acid that encodes a PRO
CC polypeptide. The nucleic acids and polypeptides are useful for treating
CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury,
CC infertility, birth defects, premature aging, acquired immunodeficiency
CC syndrome (AIDS), cancer, differentiation disorders, cell adhesion
CC disorders, neural receptor disorders, skin disorders or diabetic
CC complications. The nucleic acids are useful as hybridisation probes, in
CC chromosome and gene mapping and in generating antisense RNA or DNA. The
CC polypeptides are useful as pharmaceuticals, diagnostics, biosensors or
CC bioreactors. Both are useful in tissue typing. The present sequence
CC represents the amino acid sequence of a PRO polypeptide of the invention
XX
XX Sequence 223 AA;
XX
Qy Query Match 100.0%; Score 1204; DB 6; Length 223;
Db Best Local Similarity 100.0%; Pred. No. 7.3e-128;
Qy 1 MGWTRLVTAALLGLMMVVTGDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
Db 1 MGWTRLVTAALLGLMMVVTGDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
Qy 61 VPDNNYRQKITSWMEPIVKFPGAVDGTATVILVMVDPDAPSPRAEPQRFRHRLVTDIKG 120
Db 61 VPDNNYRQKITSWMEPIVKFPGAVDGTATVILVMVDPDAPSPRAEPQRFRHRLVTDIKG 120
Qy 121 ADLKGKIQGQELSAQAPSPPAHSGFHRVYQFFVYLQEGKVISLLPKENKTRGSWKMDRF 180
Db 121 ADLKGKIQGQELSAQAPSPPAHSGFHRVYQFFVYLQEGKVISLLPKENKTRGSWKMDRF 180
Qy 181 LNRFHGLGEPEASTQFTMTQNTQDSPTLQAPRGRASEPKHKTRQR 223
Db 181 LNRFHGLGEPEASTQFTMTQNTQDSPTLQAPRGRASEPKHKTRQR 223

RESULT 12
ADA76586
ID ADA76586 standard; protein; 223 AA.
XX
AC ADA76586;
XX
DT 20-NOV-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO4408.
XX
KW human; secreted and transmembrane protein; PRO; tumour; gene therapy;
KW tissue typing; chromosome identification; cytostatic.
XX
OS Homo sapiens.
XX
XX US2003036114-A1.
XX
XX 20-FEB-2003.
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XX 26-DEC-2001; 2001US-00035719.
PR 15-MAY-1998; 98US-0085579P.
PR 15-DEC-1998; 98US-0112514P.
PR 22-DEC-1998; 98US-0113300P.
PR 23-DEC-1998; 98US-0113430P.
PR 23-DEC-1998; 98US-0113605P.
PR 23-DEC-1998; 98US-0113621P.
PR 23-DEC-1998; 98US-0114140P.
PR 12-JAN-1999; 99US-0115552P.
PR 22-JAN-1999; 99US-0116843P.
PR 23-MAR-1999; 99US-0125774P.
PR 23-MAR-1999; 99US-0125778P.
PR 23-MAR-1999; 99US-0125826P.
PR 31-MAR-1999; 99US-0127035P.
PR 05-APR-1999; 99US-0127706P.
PR 13-APR-1999; 99US-0129122P.
PR 21-APR-1999; 99US-0130359P.
PR 27-APR-1999; 99US-0131270P.
PR 27-APR-1999; 99US-0131272P.
PR 27-APR-1999; 99US-0131291P.
PR 04-MAY-1999; 99US-0132371P.
PR 04-MAY-1999; 99US-0132379P.
PR 04-MAY-1999; 99US-0132383P.
PR 14-MAY-1999; 99US-0132383P.
PR 14-MAY-1999; 99US-0132383P.
PR 25-MAY-1999; 99US-0132383P.
PR 08-JUN-1999; 99US-0138166P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99US-02028551.
PR 22-DEC-1999; 99US-02030720.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US023678.
PR 28-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 16-AUG-2001; 2001US-00931836.
XX (GETH) GENENTECH INC.
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-615764/58.
XX N-PSDB; ADA76585.
XX Novel isolated secreted and transmembrane polypeptides, designated as PRO
PT polypeptides e.g. PRO484, PRO434 and PRO1122, useful for inhibiting
PT tumor cell growth, and for preparing medicaments for therapeutic use.
XX Claim 12; Fig 30; 201pp; English.
XX The invention describes an isolated secreted and transmembrane PRO
CC polypeptide (I), having at least 80% identity to or scoring at least 80%
CC positives when compared to, a sequence (SI) comprising 246, 440, 197, 97,
CC 273, 571, 209, 888, 310, 251, 800, 507, 248, 223, 134, 136, 468,
CC 328, 221, 194, 899, or 339 amino acids fully defined in the
CC specification. An anti-(I)-antibody is useful for determining the
CC presence of (I) in a cell. (I) is useful for identifying a compound
CC capable of inhibiting the expression and/or activity of (I). (I) and the
CC antibody are useful for inhibiting the growth of tumor cells, and for
CC the preparation of a medicament useful in the treatment of a condition
CC which is responsive to (I) or the antibody. A polynucleotide (II)

CC encoding (I) is also useful for isolating full-length PRO cDNA for
CC generating transgenic animals or knock-out animals, which are, in turn,
CC are useful in the development in the screening of therapeutically useful
CC reagents, and in gene therapy. PRO is useful in assays to identify other
CC proteins or molecules involved in binding interactions, for screening
CC inhibitors or agonists of binding interactions and for screening chemical
CC libraries. (I) is useful as molecular weight marker for protein
CC electrophoresis, and as therapeutic agents. (I) or (II) is useful for
CC tissue typing and for chromosome identification. Ab is useful in
CC diagnostic assays for PRO, in affinity purification of PRO, and for
CC detection of PRO in biological samples. This is the amino acid sequence
CC of a novel human secreted and transmembrane PRO polypeptide.
XX
SQ Sequence 223 AA;
Query Match 100.0%; Score 1204; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.3e-128;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGMTMLVTAALLGLMMVVTGDENSPCAEHALDEDTLFCQGLEVFYFELGNIGCKV 60
DB 1 MGMTMLVTAALLGLMMVVTGDENSPCAEHALDEDTLFCQGLEVFYFELGNIGCKV 60
QY 61 VPDNNYRQKITSMWEPVVKFPGAVDGYILVMVDPDAPSPRAEPQRFWRHMLVTDIKG 120
DB 61 VPDNNYRQKITSMWEPVVKFPGAVDGYILVMVDPDAPSPRAEPQRFWRHMLVTDIKG 120
QY 121 ADLKGKIQOELSAQAPSPAHSGFHRYPVYLOEGKVISLLPKENKTRGSKWMDRF 180
DB 121 ADLKGKIQOELSAQAPSPAHSGFHRYPVYLOEGKVISLLPKENKTRGSKWMDRF 180
QY 181 LNRPHLGEPEASTQFNTQYQDSPTLQAPGRASEPKHKTRQR 223
DB 181 LNRPHLGEPEASTQFNTQYQDSPTLQAPGRASEPKHKTRQR 223
RESULT 13
ABQ72343
ID ABQ72343 standard; protein; 223 AA.
XX AC ABQ72343;
XX DT 06-NOV-2003 (first entry)
XX DE Human PRO4408 protein.
XX KW PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte;
XX KW differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
XX OS Homo sapiens.
XX PN US2003050448-A1.
XX PD 13-MAR-2003.
XX PF 28-AUG-2002; 2002US-00230414.
XX PR 01-JUN-2001; 2001WO-US017800.
XX PR 29-JUN-2001; 2001WO-US021066.
XX PR 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-521818/49.
XX N-PSDB; ABT44341.
XX New nucleic acid encoding for a PRO protein, useful for the manufacture
PT of a medicament for diagnosing or treating tumors or for measuring or
PT detecting expression of an associated gene.
XX


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PS Claim 11; Fig 232; 315pp; English.
XX
CC The invention relates to a novel isolated nucleic acid encoding a fully
CC defined PRO polypeptide. The molecules of the invention may be useful for
CC stimulating proliferation or gene expression in pericyte cells or the
CC release of TNF-alpha from human blood. Other possible uses include the
CC stimulation or inhibition of chondrocyte proliferation or
CC differentiation, the stimulation of human dermal fibroblast cell
CC proliferation and the detection of the presence of a tumour within a
CC mammal. Furthermore, the nucleic acid may be useful for the manufacture
CC of a medicament for diagnosing or treating a tumour within a mammal or
CC for measuring or detecting the expression of an associated gene, as well
CC as during gene therapy. The current sequence is that of the human PRO
CC protein of the invention
XX
SQ Sequence 223 AA;
Query Match 100.0%; Score 1204; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.3e-128;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGMTMLVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
DB 1 MGMTMLVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
QY 61 VPCNNYRQKITSMWEPVVKFPGAVDGTATYLVVMDPDAPSRAEPRQRFWRHMLVTDIKG 120
DB 61 VPCNNYRQKITSMWEPVVKFPGAVDGTATYLVVMDPDAPSRAEPRQRFWRHMLVTDIKG 120
QY 121 ADLKKGKIQOELSAYQAPSPPAHSGFHRFYQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
DB 121 ADLKKGKIQOELSAYQAPSPPAHSGFHRFYQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
QY 181 LNRFLHGEPEASTQFTQNTQYQDSPTLQAPRGRASEPKHKTRQR 223
DB 181 LNRFLHGEPEASTQFTQNTQYQDSPTLQAPRGRASEPKHKTRQR 223
RESULT 14
ABJ72471
ID ABJ72471 standard; protein; 223 AA.
XX
AC ABJ72471;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human PRO4408 protein.
XX
KW PRO; blood; proliferation; pericyte cell; TNF alpha; chondrocyte;
KW tumour necrosis factor; proliferation; differentiation; gene therapy;
KW dermal fibroblast.
XX
OS Homo sapiens.
XX
PN US2003027988-A1.
XX
PD 06-FEB-2003.
XX
PF 26-AUG-2002; 2002US-00227884.
XX
PR 01-JUN-2001; 2001WO-US017800.
XX
PR 29-JUN-2001; 2001WO-US021066.
XX
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-503301/47.
XX DR N-PSDB; ABT44624.
XX
XX New PRO protein encoding nucleic acid, useful for preparing PRO
PT
```

```
PT polypeptides and anti-PRO antibodies for detecting the presence of a
PT tumor in a mammal.
XX
XX Claim 11; Fig 232; 324pp; English.
XX
CC The invention relates to a novel isolated PRO protein encoding nucleic
CC acid. The nucleic acid of the invention may be useful for preparing PRO
CC polypeptides and anti-PRO antibodies for detecting the presence of a
CC tumour in a mammal. Furthermore, the molecules of the invention may be
CC useful for stimulating proliferation or gene expression in pericyte
CC cells, the release of tumour necrosis factor (TNF)-alpha from human
CC blood, the proliferation or differentiation of chondrocyte cells and for
CC inhibiting the proliferation of normal human dermal fibroblast cells.
CC Finally, the molecules may be utilised during gene therapy. The current
CC sequence is that of the human PRO protein of the invention
XX
SQ Sequence 223 AA;
Query Match 100.0%; Score 1204; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.3e-128;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGMTMLVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
DB 1 MGMTMLVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
QY 61 VPCNNYRQKITSMWEPVVKFPGAVDGTATYLVVMDPDAPSRAEPRQRFWRHMLVTDIKG 120
DB 61 VPCNNYRQKITSMWEPVVKFPGAVDGTATYLVVMDPDAPSRAEPRQRFWRHMLVTDIKG 120
QY 121 ADLKKGKIQOELSAYQAPSPPAHSGFHRFYQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
DB 121 ADLKKGKIQOELSAYQAPSPPAHSGFHRFYQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
QY 181 LNRFLHGEPEASTQFTQNTQYQDSPTLQAPRGRASEPKHKTRQR 223
DB 181 LNRFLHGEPEASTQFTQNTQYQDSPTLQAPRGRASEPKHKTRQR 223
RESULT 15
ABO34366
ID ABO34366 standard; protein; 223 AA.
XX
AC ABO34366;
XX
DT 19-SEP-2003 (first entry)
XX
DE Human secreted/transmembrane polypeptide PRO 4405.
XX
KW Human; chondrocyte stimulation; TNF-alpha stimulation; gene therapy;
KW human dermal fibroblast stimulation; tumour; tissue typing;
KW affinity purification.
XX
OS Homo sapiens.
XX
PN US2003044934-A1.
XX
PD 06-MAR-2003.
XX
PF 28-AUG-2002; 2002US-00230338.
XX
PR 01-JUN-2001; 2001WO-US017800.
XX
PR 29-JUN-2001; 2001WO-US021066.
XX
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-492274/46.
XX DR N-PSDB; AC082291.
XX
```

PT New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
XX chromosome markers, or in generating probes.
PS
XX Claim 19; Fig 232; 315pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. Nucleic acids that encode PRO can be used to generate either
CC transgenic animals or knock-out animals useful in developing and
CC screening of therapeutically useful reagents. The nucleic acids may also
CC be used in gene therapy for replacing defective gene, in chromosome
CC identification, as chromosome markers, or in generating probes to isolate
CC full length PRO cDNA. The PRO polypeptides are useful for chondrocyte
CC stimulation, TNF-alpha stimulation, human dermal fibroblasts stimulation
CC and for detecting the presence of tumour in an mammal. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The present sequence represents the amino acid sequence
XX of a human secreted/transmembrane PRO polypeptide
SQ Sequence 223 AA;

Query Match 100.0%; Score 1204; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.3e-128;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGMTMLRVTAALLGLMMVVTGDEDNPCAEHALDDETLFCQGLEVFYFPELGNIGCKV 60
Db 1 MGMTMLRVTAALLGLMMVVTGDEDNPCAEHALDDETLFCQGLEVFYFPELGNIGCKV 60

Qy 61 VPCNNYRQKITSMEPIVKFPGAVDGCATYILVMVDPDAPSPRAEPQRQRFWRHVLVTDIKG 120
Db 61 VPCNNYRQKITSMEPIVKFPGAVDGCATYILVMVDPDAPSPRAEPQRQRFWRHVLVTDIKG 120

Qy 121 ADLKKGIQGELSAYQAPSPRAHSGFPHRYQFFVYLOEGKVISLLPKENKTRGSWKMDRF 180
Db 121 ADLKKGIQGELSAYQAPSPRAHSGFPHRYQFFVYLOEGKVISLLPKENKTRGSWKMDRF 180

Qy 181 LNRPHLGEPEASTQFTQNYQDSPTLQAPRGRASEPKHKTRQR 223
Db 181 LNRPHLGEPEASTQFTQNYQDSPTLQAPRGRASEPKHKTRQR 223

Search completed: January 30, 2005, 17:07:54
Job time : 188 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 30, 2005, 16:56:53 ; Search time 28 Seconds
(without alignments)
528.176 Million cell updates/sec

Title: US-10-035-958-61

Perfect score: 1204

Sequence: 1 MGWMLVTAALLGLMMVV.....PTLOAPRGRASEPKHYRQR 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1181	98.1	227	3	US-09-208-718-3
2	1177	97.8	227	4	US-09-621-976-8
3	1177	97.8	227	4	US-09-513-999C-8
4	235.5	19.6	187	4	US-09-492-308A-7
5	231	19.2	152	3	US-09-208-718-6
6	218.5	18.1	186	4	US-09-492-308A-8
7	210.5	17.5	187	1	US-08-403-378B-4
8	205	17.0	187	1	US-08-403-378B-15
9	164	13.6	175	3	US-09-060-726A-2
10	164	13.6	175	4	US-09-845-849A-2
11	161.5	13.4	141	4	US-09-270-767-43926
12	157	13.0	272	4	US-09-248-796A-16385
13	148	12.3	181	4	US-09-492-308A-2
14	142.5	11.8	177	4	US-09-492-308A-23
15	139	11.5	152	1	US-07-644-372-2
16	137.5	11.4	120	4	US-09-270-767-33653
17	137.5	11.4	120	4	US-09-270-767-48870
18	137.5	11.4	177	4	US-09-492-308A-5
19	137.5	11.4	177	4	US-09-492-308A-22
20	131.5	10.9	177	4	US-09-492-308A-21
21	130.5	10.8	177	4	US-09-492-308A-20
22	102.5	8.5	115	4	US-09-845-849A-8
23	99.5	8.3	132	4	US-09-270-767-57507
24	99.5	8.3	268	4	US-09-270-767-42230
25	96.5	8.0	104	3	US-09-060-726A-6
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27	92.5	7.7	172	4	US-09-902-331B-10
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Sequence 80, Appli
Sequence 943, App
Sequence 2, Appli
Sequence 16, Appli
Sequence 9, Appli
Sequence 15, Appli
Sequence 13170, A
Sequence 2, Appli
Sequence 4, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 4167, Ap
Sequence 6066, Ap
Sequence 79, Appli
Sequence 6758, Ap
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Sequence 25, Appli
Sequence 25, Appli
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Sequence 25, Appli
Sequence 3, Appli
Sequence 3, Appli
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Sequence 6, Appli
Sequence 4, Appli
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Sequence 58, Appli
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Sequence 4, Appli
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Sequence 14, Appli
Sequence 2, Appli
Sequence 22158, A
Sequence 53, Appli
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Sequence 31, Appli
Sequence 45190, A
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Sequence 2031, A
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Sequence 12, Appli
Sequence 32, Appli
Sequence 39, Appli

101	69	5.7	214	5	PCT-US93-07832-39	Sequence 39, Appl	174	66	5.5	2089	1	US-08-418-893D-24	Sequence 24, Appl
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103	69	5.7	361	4	US-09-585-858-35	Sequence 35, Appl	176	65.5	5.4	279	3	US-09-318-794A-3	Sequence 3, Appl
104	69	5.7	1064	4	US-09-626-301-4	Sequence 4, Appl	177	65.5	5.4	279	3	US-09-318-794A-5	Sequence 5, Appl
105	68.5	5.7	343	4	US-09-360-376-17	Sequence 17, Appl	178	65.5	5.4	297	3	US-09-187-049-10	Sequence 10, Appl
106	68.5	5.7	472	1	US-08-203-005B-14	Sequence 14, Appl	179	65.5	5.4	379	4	US-09-402-532-1	Sequence 1, Appl
107	68.5	5.7	551	4	US-09-489-039A-14227	Sequence 14227, A	180	65.5	5.4	382	4	US-09-402-532-4	Sequence 4, Appl
108	68.5	5.7	605	4	US-09-832-496-2	Sequence 2, Appl	181	65.5	5.4	401	4	US-09-864-894C-1	Sequence 1, Appl
109	68.5	5.7	605	4	US-09-832-616-2	Sequence 2, Appl	182	65.5	5.4	427	4	US-10-179-784-3	Sequence 3, Appl
110	68	5.6	214	1	US-08-425-763-1	Sequence 1, Appl	183	65.5	5.4	454	4	US-09-252-991A-28716	Sequence 28716, A
111	68	5.6	214	3	US-08-811-757-1	Sequence 1, Appl	184	65.5	5.4	487	4	US-09-691-344A-2	Sequence 2, Appl
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113	68	5.6	229	3	US-09-045-973-7	Sequence 7, Appl	186	65.5	5.4	586	4	US-09-691-344A-4	Sequence 4, Appl
114	68	5.6	233	4	US-08-030-175-43	Sequence 43, Appl	187	65.5	5.4	587	4	US-09-107-531A-6405	Sequence 6405, Ap
115	68	5.6	259	4	US-09-252-991A-31123	Sequence 31123, A	188	65.5	5.4	706	4	US-09-252-991A-24766	Sequence 24766, A
116	68	5.6	474	2	US-08-282-197C-58	Sequence 58, Appl	189	65.5	5.4	828	4	US-09-248-796A-20746	Sequence 20746, A
117	68	5.6	475	4	US-09-054-272-40	Sequence 40, Appl	190	65	5.4	364	4	US-09-489-039A-12968	Sequence 12968, A
118	68	5.6	585	4	US-09-462-951B-1	Sequence 1, Appl	191	65	5.4	445	4	US-09-252-991A-18993	Sequence 18993, A
119	68	5.6	2476	2	US-08-276-967-2	Sequence 2, Appl	192	65	5.4	449	4	US-09-984-880-2	Sequence 2, Appl
120	67.5	5.6	154	4	US-09-270-767-47410	Sequence 47410, A	193	65	5.4	449	4	US-10-277-032-2	Sequence 2, Appl
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122	67.5	5.6	472	3	US-09-088-641-4	Sequence 4, Appl	195	65	5.4	574	4	US-09-489-039A-13400	Sequence 13400, A
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124	67.5	5.6	512	2	US-08-265-310-4	Sequence 4, Appl	197	65	5.4	877	2	US-08-907-166-8	Sequence 8, Appl
125	67.5	5.6	512	3	US-08-951-742-4	Sequence 4, Appl	198	65	5.4	877	2	US-09-391-340-8	Sequence 8, Appl
126	67.5	5.6	596	3	US-08-481-190-8	Sequence 8, Appl	199	65	5.4	951	4	US-09-125-635-8	Sequence 8, Appl
127	67.5	5.6	596	3	PCT-US93-00869-8	Sequence 8, Appl	200	65	5.4	983	3	US-09-412-554A-2	Sequence 2, Appl
128	67.5	5.6	610	4	US-09-248-796A-17030	Sequence 17030, A	201	65	5.4	1296	4	US-08-857-636-60	Sequence 60, Appl
129	67.5	5.6	921	3	US-09-514-599-2	Sequence 2, Appl	202	65	5.4	1420	4	US-09-125-635-4	Sequence 4, Appl
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131	67	5.6	158	3	US-08-411-768B-5	Sequence 5, Appl	204	65	5.4	1434	3	US-08-656-055-10	Sequence 10, Appl
132	67	5.6	214	2	US-07-934-373C-24	Sequence 24, Appl	205	65	5.4	1434	3	US-08-954-668-10	Sequence 10, Appl
133	67	5.6	214	3	US-08-437-642B-24	Sequence 24, Appl	206	65	5.4	1434	4	US-08-918-658-10	Sequence 10, Appl
134	67	5.6	214	4	US-08-146-206C-24	Sequence 24, Appl	207	65	5.4	1434	4	US-09-724-631-10	Sequence 10, Appl
135	67	5.6	214	4	US-09-705-686-24	Sequence 24, Appl	208	65	5.4	1434	4	US-08-954-701A-10	Sequence 10, Appl
136	67	5.6	214	4	PCT-US93-07832-24	Sequence 24, Appl	209	65	5.4	1447	5	PCT-US95-13233-10	Sequence 10, Appl
137	67	5.6	214	5	US-09-705-392A-24	Sequence 24, Appl	210	65	5.4	1447	2	US-08-540-406-19	Sequence 19, Appl
138	67	5.6	228	3	US-09-181-958-2	Sequence 2, Appl	211	65	5.4	1447	3	US-08-656-055-19	Sequence 19, Appl
139	67	5.6	347	4	US-09-268-544B-38	Sequence 38, Appl	212	65	5.4	1447	3	US-08-954-668-19	Sequence 19, Appl
140	67	5.6	372	1	US-08-403-634-2	Sequence 2, Appl	213	65	5.4	1447	3	US-09-268-140-5	Sequence 5, Appl
141	67	5.6	372	1	US-08-403-634-30	Sequence 30, Appl	214	65	5.4	1447	4	US-08-918-658-19	Sequence 19, Appl
142	67	5.6	372	3	US-08-913-441B-2	Sequence 2, Appl	215	65	5.4	1447	4	US-09-724-631-19	Sequence 19, Appl
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144	67	5.6	388	4	US-09-543-681A-4387	Sequence 4387, Ap	217	65	5.4	1447	5	PCT-US95-13233-19	Sequence 19, Appl
145	67	5.6	412	4	US-09-402-532-6	Sequence 6, Appl	218	64.5	5.4	108	4	US-09-513-999C-4705	Sequence 4705, Ap
146	67	5.6	438	4	US-09-268-544B-36	Sequence 36, Appl	219	64.5	5.4	223	4	US-09-270-767-38681	Sequence 38681, A
147	67	5.6	465	4	US-09-720-181A-12	Sequence 12, Appl	220	64.5	5.4	223	4	US-09-270-767-53898	Sequence 53898, A
148	67	5.6	543	3	US-08-697-610-2	Sequence 2, Appl	221	64.5	5.4	285	4	US-09-710-279-174	Sequence 174, App
149	67	5.6	543	3	US-08-349-357-2	Sequence 2, Appl	222	64.5	5.4	300	4	US-09-585-858-45	Sequence 45, Appl
150	67	5.6	556	2	US-08-505-377-1	Sequence 1, Appl	223	64.5	5.4	360	4	US-09-252-991A-21624	Sequence 21624, A
151	67	5.6	556	3	US-08-798-269-1	Sequence 1, Appl	224	64.5	5.4	369	4	US-09-328-352-4297	Sequence 4297, Ap
152	67	5.6	556	3	US-09-055-210-1	Sequence 1, Appl	225	64.5	5.4	437	3	US-09-134-001C-5342	Sequence 5342, Ap
153	67	5.6	556	3	US-09-298-224-8	Sequence 8, Appl	226	64.5	5.4	501	3	US-09-167-206-3	Sequence 3, Appl
154	67	5.6	567	4	US-09-645-926A-7	Sequence 7, Appl	227	64.5	5.4	533	4	US-09-489-039A-7511	Sequence 7511, Ap
155	67	5.6	812	1	US-08-446-794A-4	Sequence 4, Appl	228	64.5	5.4	550	4	US-09-344-510B-4	Sequence 4, Appl
156	66.5	5.5	269	4	US-09-531-056A-14	Sequence 14, Appl	229	64.5	5.4	707	1	US-08-803-973-12	Sequence 12, Appl
157	66.5	5.5	285	3	US-09-289-349-12	Sequence 12, Appl	230	64.5	5.4	707	1	US-08-803-972-12	Sequence 12, Appl
158	66.5	5.5	328	4	US-09-531-056A-13	Sequence 13, Appl	231	64.5	5.4	812	1	US-08-446-794A-2	Sequence 2, Appl
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160	66.5	5.5	398	4	US-09-489-039A-10213	Sequence 10213, A	233	64.5	5.4	812	2	US-08-945-024-2	Sequence 2, Appl
161	66.5	5.5	451	3	US-08-878-177-2	Sequence 2, Appl	234	64.5	5.4	834	4	US-09-252-991A-28145	Sequence 28145, A
162	66.5	5.5	514	4	US-09-252-991A-28208	Sequence 2, Appl	235	64.5	5.4	1014	4	US-09-344-510B-3	Sequence 3, Appl
163	66.5	5.5	660	4	US-09-252-991A-32206	Sequence 32206, A	236	64.5	5.4	1172	4	US-09-328-352-6071	Sequence 6071, Ap
164	66.5	5.5	1008	4	US-09-252-991A-29419	Sequence 29419, A	237	64	5.3	214	2	US-07-934-373C-40	Sequence 40, Appl
165	66	5.5	114	4	US-09-845-849A-5	Sequence 5, Appl	238	64	5.3	214	2	US-08-788-800-11	Sequence 11, Appl
166	66	5.5	233	4	US-09-252-991A-32770	Sequence 32770, A	239	64	5.3	214	3	US-08-437-642B-40	Sequence 40, Appl
167	66	5.5	277	4	US-09-107-532A-7213	Sequence 7213, Ap	240	64	5.3	214	3	US-09-097-309-2	Sequence 2, Appl
168	66	5.5	462	4	US-09-252-991A-18530	Sequence 18530	241	64	5.3	214	3	US-09-097-171A-2	Sequence 2, Appl
169	66	5.5	746	4	US-09-370-838-185	Sequence 185, App	242	64	5.3	214	3	US-09-460-587-2	Sequence 2, Appl
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171	66	5.5	1116	4	US-09-252-991A-24374	Sequence 24374, A	244	64	5.3	216	5	PCT-US93-07832-40	Sequence 40, Appl
172	66	5.5	1467	4	US-09-134-000C-6740	Sequence 6740, Ap	245	64	5.3	216	2	US-08-821-637-3	Sequence 3, Appl
173	66	5.5	2089	1	US-08-418-893D-23	Sequence 23, Appl	246	64	5.3	216	4	US-09-215-160-3	Sequence 3, Appl

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248	64	5.3	237	3	US-09-097-171A-10	Sequence 10, Appl	321	63	5.2	622	3	US-09-305-381-2	Sequence 2, Appli
249	64	5.3	237	3	US-09-422-712B-2	Sequence 2, Appli	322	63	5.2	725	4	US-09-252-991A-23752	Sequence 2, Appli
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257	64	5.3	449	4	US-09-198-452A-1114	Sequence 1114, Ap	330	63	5.2	879	1	US-08-413-118-106	Sequence 106, App
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261	64	5.3	555	2	US-08-687-852-6	Sequence 6, Appli	334	63	5.2	1085	1	US-08-485-588-5	Sequence 5, Appli
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265	63.5	5.3	230	4	US-09-248-796A-18983	Sequence 18983, A	338	63	5.2	1085	3	US-08-353-784-5	Sequence 5, Appli
266	63.5	5.3	235	3	US-09-423-439-18	Sequence 18, Appl	339	63	5.2	1085	3	US-08-484-719B-5	Sequence 5, Appli
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268	63.5	5.3	239	3	US-08-749-699-44	Sequence 44, Appl	341	63	5.2	1151	4	US-09-710-279-2448	Sequence 2448, Ap
269	63.5	5.3	239	4	US-09-004-729-44	Sequence 44, Appl	342	63	5.2	1154	3	US-09-134-001C-3428	Sequence 3428, Ap
270	63.5	5.3	242	3	US-09-004-731-41	Sequence 41, Appl	343	63	5.2	1481	3	US-09-251-645-14	Sequence 14, Appl
271	63.5	5.3	242	3	US-09-032-215-47	Sequence 47, Appl	344	62.5	5.2	134	4	US-09-252-991A-23154	Sequence 23154, A
272	63.5	5.3	242	3	US-08-749-699-41	Sequence 41, Appl	345	62.5	5.2	214	2	US-08-480-753-6	Sequence 6, Appl
273	63.5	5.3	242	4	US-09-004-729-41	Sequence 41, Appl	346	62.5	5.2	214	3	US-09-041-889-11	Sequence 11, Appl
274	63.5	5.3	300	3	US-08-158-735A-17	Sequence 17, Appl	347	62.5	5.2	214	3	US-08-837-058-11	Sequence 11, Appl
275	63.5	5.3	314	4	US-09-360-376-14	Sequence 14, Appl	348	62.5	5.2	214	4	US-09-417-264-11	Sequence 11, Appl
276	63.5	5.3	358	3	US-09-821-736-4	Sequence 4, Appli	349	62.5	5.2	220	4	US-09-134-000C-6778	Sequence 6778, Ap
277	63.5	5.3	334	4	US-09-252-991A-32042	Sequence 32042, A	350	62.5	5.2	233	3	US-09-485-737B-69	Sequence 69, Appl
278	63.5	5.3	431	4	US-09-252-991A-28694	Sequence 28694, A	351	62.5	5.2	265	4	US-09-489-039A-12711	Sequence 12711, A
279	63.5	5.3	501	1	US-08-149-105-17	Sequence 17, Appl	352	62.5	5.2	328	4	US-09-583-110-4999	Sequence 4999, Ap
280	63.5	5.3	501	1	US-08-317-847-17	Sequence 17, Appl	353	62.5	5.2	344	3	US-09-120-365-63	Sequence 63, Appl
281	63.5	5.3	503	3	US-09-382-256-10	Sequence 10, Appl	354	62.5	5.2	344	3	US-09-515-039-63	Sequence 63, Appl
282	63.5	5.3	503	3	US-09-395-115-10	Sequence 10, Appl	355	62.5	5.2	345	4	US-09-270-767-60654	Sequence 60654, A
283	63.5	5.3	503	3	US-08-123-934A-10	Sequence 10, Appl	356	62.5	5.2	404	4	US-09-270-767-45164	Sequence 45164, A
284	63.5	5.3	503	3	US-08-436-265-10	Sequence 10, Appl	357	62.5	5.2	592	3	US-09-328-352-4438	Sequence 4438, Ap
285	63.5	5.3	503	3	US-09-679-187-10	Sequence 10, Appl	358	62.5	5.2	593	3	US-09-000-145-4	Sequence 4, Appli
286	63.5	5.3	503	4	US-09-874-628-10	Sequence 10, Appl	359	62.5	5.2	603	4	US-09-252-991A-25038	Sequence 25038, A
287	63.5	5.3	503	4	US-09-267-963D-10	Sequence 10, Appl	360	62.5	5.2	688	4	US-09-538-092-794	Sequence 794, App
288	63.5	5.3	518	4	US-09-248-796A-18577	Sequence 18577, A	361	62.5	5.2	858	4	US-09-538-092-1127	Sequence 1127, Ap
289	63.5	5.3	518	4	US-09-248-796A-18577	Sequence 18577, A	362	62.5	5.2	898	4	US-09-583-110-3750	Sequence 3750, Ap
290	63.5	5.3	636	4	US-09-489-039A-13947	Sequence 13947, A	363	62.5	5.2	1028	4	US-09-583-110-4280	Sequence 4280, Ap
291	63.5	5.3	674	1	US-08-803-973-7	Sequence 7, Appli	364	62.5	5.2	1068	2	US-08-429-054A-11	Sequence 11, Appl
292	63.5	5.3	674	1	US-08-803-972-7	Sequence 7, Appli	365	62.5	5.2	1068	2	US-08-718-777-7	Sequence 7, Appli
293	63.5	5.3	753	4	US-09-248-796A-19041	Sequence 19041, A	366	62.5	5.2	1068	3	US-09-051-341-7	Sequence 7, Appli
294	63.5	5.3	786	4	US-09-543-681A-6650	Sequence 6650, Ap	367	62.5	5.2	1068	4	US-09-394-272-8	Sequence 8, Appli
295	63.5	5.3	1286	6	5208163-1	Patent No. 5208163	368	62.5	5.2	1068	4	US-08-429-053-11	Sequence 11, Appl
296	63.5	5.3	1456	1	US-08-803-973-2	Sequence 2, Appli	369	62.5	5.2	2285	4	US-09-252-991A-17790	Sequence 17790, A
297	63.5	5.3	1456	1	US-08-803-972-2	Sequence 2, Appli	370	62	5.1	69	3	US-09-060-726A-7	Sequence 7, Appli
298	63.5	5.3	2627	2	US-08-751-189-3	Sequence 3, Appli	371	62	5.1	72	4	US-09-845-849A-7	Sequence 7, Appli
299	63.5	5.3	2627	2	US-09-060-836-3	Sequence 3, Appli	372	62	5.1	176	4	US-09-252-991A-30933	Sequence 30933, A
300	63.5	5.3	2627	3	US-09-184-445-3	Sequence 3, Appli	373	62	5.1	218	4	US-09-134-000C-4932	Sequence 4932, Ap
301	63	5.2	113	4	US-09-621-976-4206	Sequence 4206, Ap	374	62	5.1	455	3	US-08-679-638A-5	Sequence 5, Appli
302	63	5.2	206	1	US-08-097-827-7	Sequence 7, Appli	375	62	5.1	455	3	US-09-419-163-5	Sequence 5, Appli
303	63	5.2	206	1	US-08-494-574-7	Sequence 7, Appli	376	62	5.1	554	4	US-09-198-452A-140	Sequence 140, App
304	63	5.2	239	4	US-09-543-681A-7402	Sequence 7402, Ap	377	62	5.1	621	4	US-09-489-039A-13909	Sequence 13909, A
305	63	5.2	293	3	US-09-512-342-14	Sequence 14, Appl	378	62	5.1	663	4	US-09-252-991A-30843	Sequence 30843, A
306	63	5.2	301	4	US-09-107-532A-4953	Sequence 4953, Ap	379	62	5.1	706	1	US-08-074-967-2	Sequence 2, Appli
307	63	5.2	336	4	US-09-489-039A-13630	Sequence 13630, A	380	62	5.1	706	2	US-08-553-541B-2	Sequence 2, Appli
308	63	5.2	417	4	US-09-248-796A-19586	Sequence 19586, A	381	62	5.1	706	3	US-09-268-202-2	Sequence 2, Appli
309	63	5.2	419	4	US-09-252-991A-22888	Sequence 22888, A	382	62	5.1	706	3	US-09-761-117-2	Sequence 2, Appli
310	63	5.2	438	1	US-08-097-827-11	Sequence 11, Appl	383	62	5.1	706	5	US-09-252-991A-24589	Sequence 24589, A
311	63	5.2	438	1	US-08-494-574-11	Sequence 11, Appl	384	62	5.1	755	3	US-09-929-329-5	Sequence 5, Appli
312	63	5.2	478	3	US-08-878-177-4	Sequence 4, Appli	385	62	5.1	826	4	US-09-097-767A-38	Sequence 38, Appl
313	63	5.2	485	3	US-09-651-941-9	Sequence 9, Appli	386	62	5.1	843	4	US-09-134-000C-4999	Sequence 4999, Ap
314	63	5.2	485	4	US-09-955-597-9	Sequence 9, Appli	387	62	5.1	843	4	US-09-252-991A-32609	Sequence 32609, A
315	63	5.2	498	4	US-09-786-240-1	Sequence 1, Appli	388	62	5.1	1130	4	US-09-538-092-834	Sequence 834, App
316	63	5.2	508	3	US-09-655-270A-9	Sequence 9, Appli	389	62	5.1	1286	4	US-09-252-991A-24589	Sequence 24589, A
317	63	5.2	528	3	US-08-304-871-5	Sequence 5, Appli	390	61.5	5.1	1507	3	US-08-929-329-5	Sequence 5, Appli
318	63	5.2	546	2	US-08-492-027A-8	Sequence 8, Appli	391	61.5	5.1	235	4	US-09-011-769A-27	Sequence 27, Appl
319	63	5.2	546	4	US-09-832-441-2	Sequence 2, Appli	392	61.5	5.1	236	4	US-09-328-352-6285	Sequence 6285, Ap
320	63	5.2	599	4						271	1	US-07-914-282D-64	Sequence 4, Appli

393	61.5	5.1	271	1	US-08-276-887A-4	Sequence 4, Appli	466	60.5	5.0	205	4	US-09-906-700-23	Sequence 23, Appli
394	61.5	5.1	271	5	PCT-US93-02460-4	Sequence 4, Appli	467	60.5	5.0	205	4	US-10-140-002-274	Sequence 274, App
395	61.5	5.1	285	4	US-09-252-991A-29780	Sequence 12760, A	468	60.5	5.0	205	4	US-09-903-603A-23	Sequence 23, Appli
396	61.5	5.1	292	4	US-09-489-039A-12760	Sequence 12760, A	469	60.5	5.0	212	3	US-09-036-985A-2	Sequence 2, Appli
397	61.5	5.1	297	4	US-09-543-681A-8242	Sequence 16242, A	470	60.5	5.0	224	4	US-09-456-090A-40	Sequence 40, Appli
398	61.5	5.1	349	4	US-09-248-796A-16744	Sequence 16744, A	471	60.5	5.0	224	4	US-09-453-234-40	Sequence 40, Appli
399	61.5	5.1	388	4	US-09-252-991A-21572	Sequence 21572, A	472	60.5	5.0	239	3	US-08-812-586-29	Sequence 29, Appli
400	61.5	5.1	414	4	US-09-248-796A-19046	Sequence 19046, A	473	60.5	5.0	239	4	US-09-535-832A-30	Sequence 30, Appli
401	61.5	5.1	457	3	US-08-431-517F-14	Sequence 14, Appli	474	60.5	5.0	258	4	US-09-328-352-8149	Sequence 8149, Ap
402	61.5	5.1	472	3	US-09-088-641-5	Sequence 5, Appli	475	60.5	5.0	370	2	US-08-341-538A-2	Sequence 2, Appli
403	61.5	5.1	472	3	US-09-088-641-5	Sequence 5, Appli	476	60.5	5.0	370	2	US-08-725-518-2	Sequence 2, Appli
404	61.5	5.1	569	4	US-09-514-245-22	Sequence 13, Appli	477	60.5	5.0	370	4	US-09-538-092-1286	Sequence 1286, Ap
405	61.5	5.1	612	4	US-09-248-796A-15682	Sequence 22, Appli	478	60.5	5.0	380	3	US-08-468-846-2	Sequence 2, Appli
406	61.5	5.1	612	4	US-09-248-796A-15682	Sequence 22, Appli	479	60.5	5.0	380	3	US-08-915-096A-2	Sequence 2, Appli
407	61.5	5.1	617	4	US-09-252-991A-29507	Sequence 29507, A	480	60.5	5.0	381	4	US-09-248-796A-16356	Sequence 16356, A
408	61.5	5.1	727	4	US-09-585-858-32	Sequence 32, Appli	481	60.5	5.0	386	4	US-09-248-796A-17565	Sequence 17565, A
409	61.5	5.1	775	1	US-07-966-278-1	Sequence 1, Appli	482	60.5	5.0	427	4	US-09-248-796A-17709	Sequence 17709, A
410	61.5	5.1	775	1	US-08-424-921-1	Sequence 1, Appli	483	60.5	5.0	453	4	US-09-543-681A-6645	Sequence 6645, Ap
411	61.5	5.1	775	2	US-08-556-355A-1	Sequence 1, Appli	484	60.5	5.0	472	3	US-08-985-492-13	Sequence 13, Appli
412	61.5	5.1	775	2	US-07-803-627A-1	Sequence 1, Appli	485	60.5	5.0	541	4	US-09-252-991A-32947	Sequence 32947, A
413	61.5	5.1	775	4	US-09-244-889A-1	Sequence 1, Appli	486	60.5	5.0	579	4	US-09-252-991A-18063	Sequence 18063, A
414	61.5	5.1	776	2	US-08-688-649-37	Sequence 37, Appli	487	60.5	5.0	643	4	US-09-252-991A-17181	Sequence 17181, A
415	61.5	5.1	844	4	US-09-640-958-8	Sequence 8, Appli	488	60.5	5.0	667	3	US-08-959-004-11	Sequence 11, Appli
416	61.5	5.1	908	4	US-09-635-077A-15	Sequence 15, Appli	489	60.5	5.0	668	4	US-09-252-991A-19879	Sequence 19879, A
417	61.5	5.1	908	4	US-09-636-077A-15	Sequence 15, Appli	490	60.5	5.0	824	4	US-09-134-000C-4908	Sequence 4908, Ap
418	61.5	5.1	908	4	US-09-636-060C-15	Sequence 15, Appli	491	60.5	5.0	864	4	US-09-751-687-18	Sequence 18, Appli
419	61.5	5.1	908	4	US-09-986-552-15	Sequence 15, Appli	492	60.5	5.0	1088	4	US-09-252-991A-27278	Sequence 27278, A
420	61.5	5.1	908	4	US-09-986-552-15	Sequence 15, Appli	493	60.5	5.0	1226	1	US-08-280-443-2	Sequence 2, Appli
421	61.5	5.1	927	3	US-08-895-601-6	Sequence 6, Appli	494	60.5	5.0	1226	1	US-08-457-459-2	Sequence 2, Appli
422	61.5	5.1	1809	3	US-09-012-515A-12	Sequence 12, Appli	495	60.5	5.0	1226	1	US-08-555-678-2	Sequence 2, Appli
423	61.5	5.1	1809	3	US-08-360-144A-12	Sequence 12, Appli	496	60.5	5.0	1226	5	PCT-US95-02275-2	Sequence 2, Appli
424	61.5	5.1	1809	4	US-09-012-504A-12	Sequence 12, Appli	497	60.5	5.0	1226	5	US-09-917-254-92	Sequence 92, Appli
425	61.5	5.1	1809	4	US-09-012-399A-12	Sequence 12, Appli	498	60.5	5.0	2396	1	US-08-157-005-2	Sequence 2, Appli
426	61.5	5.1	2549	3	US-08-471-112A-3	Sequence 3, Appli	499	60.5	5.0	2396	3	US-08-747-863-2	Sequence 2, Appli
427	61.5	5.1	2549	4	US-09-950-634-3	Sequence 3, Appli	500	60.5	5.0	2396	4	US-09-565-864-2	Sequence 2, Appli
428	61.5	5.1	2549	4	US-09-538-092-1112	Sequence 1112, Ap	501	60.5	5.0	2549	4	US-08-265-967C-1	Sequence 1, Appli
429	61.5	5.1	2549	5	PCT-US95-06722-12	Sequence 12, Appli	502	60.5	5.0	2549	4	US-08-305-790B-2	Sequence 2, Appli
430	61	5.1	161	4	US-09-583-110-4752	Sequence 4752, Ap	503	60	5.0	143	4	US-09-543-681A-4427	Sequence 4427, Ap
431	61	5.1	223	4	US-09-248-796A-23094	Sequence 23094, A	504	60	5.0	186	4	US-09-540-236-3237	Sequence 3237, Ap
432	61	5.1	252	4	US-09-252-991A-30900	Sequence 30900, A	505	60	5.0	186	4	US-09-248-796A-16423	Sequence 16423, A
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434	61	5.1	359	4	US-09-489-039A-8365	Sequence 8365, Ap	507	60	5.0	352	4	US-09-134-000C-5243	Sequence 5243, Ap
435	61	5.1	368	4	US-09-252-991A-19552	Sequence 19552, A	508	60	5.0	398	2	US-08-474-379C-86	Sequence 86, Appli
436	61	5.1	383	4	US-09-248-796A-20283	Sequence 20283, A	509	60	5.0	414	4	US-09-107-532A-6114	Sequence 6114, Ap
437	61	5.1	385	4	US-09-328-352-8185	Sequence 8185, Ap	510	60	5.0	422	3	US-09-217-228-7	Sequence 7, Appli
438	61	5.1	397	5	PCT-US95-17111A-121	Sequence 121, App	511	60	5.0	424	4	US-08-311-731A-220	Sequence 220, App
439	61	5.1	495	4	US-09-252-991A-24607	Sequence 24607, A	512	60	5.0	478	4	US-09-270-767-43204	Sequence 43204, A
440	61	5.1	496	4	US-09-339-159B-28	Sequence 28, Appli	513	60	5.0	508	4	US-09-252-991A-17606	Sequence 17606, A
441	61	5.1	497	4	US-09-181-339-3	Sequence 3, Appli	514	60	5.0	513	4	US-09-595-857B-30	Sequence 30, Appli
442	61	5.1	560	2	US-08-808-931-18	Sequence 18, Appli	515	60	5.0	542	3	US-08-675-816-6	Sequence 6, Appli
443	61	5.1	560	2	US-08-808-931-18	Sequence 18, Appli	516	60	5.0	542	4	US-09-773-426A-9	Sequence 9, Appli
444	61	5.1	560	3	US-09-050-603A-18	Sequence 18, Appli	517	60	5.0	552	4	US-10-314-881-9	Sequence 9, Appli
445	61	5.1	560	3	US-09-102-420B-18	Sequence 18, Appli	518	60	5.0	559	4	US-09-252-991A-17250	Sequence 17250, A
446	61	5.1	560	3	US-09-497-698-18	Sequence 18, Appli	519	60	5.0	608	3	US-09-134-001C-3395	Sequence 3395, Ap
447	61	5.1	565	4	US-09-252-991A-28571	Sequence 28571, A	520	60	5.0	638	1	US-07-688-352C-22	Sequence 22, Appli
448	61	5.1	660	4	US-09-252-991A-22842	Sequence 22842, A	521	60	5.0	673	3	US-09-091-725-23	Sequence 23, Appli
449	61	5.1	710	1	US-08-162-809-22	Sequence 22, Appli	522	60	5.0	686	2	US-08-942-521B-9	Sequence 9, Appli
450	61	5.1	722	1	US-08-162-809-4	Sequence 4, Appli	523	60	5.0	734	3	US-09-146-249A-85	Sequence 85, Appli
451	61	5.1	744	1	US-08-162-809-20	Sequence 20, Appli	524	60	5.0	734	3	US-08-206-188B-85	Sequence 85, Appli
452	61	5.1	774	3	US-08-902-632-2	Sequence 2, Appli	525	60	5.0	886	2	US-08-474-379C-65	Sequence 65, Appli
453	61	5.1	774	3	US-09-073-354-1	Sequence 1, Appli	526	60	5.0	886	3	US-09-146-249A-65	Sequence 65, Appli
454	61	5.1	774	3	US-08-656-005A-1	Sequence 1, Appli	527	60	5.0	886	3	US-08-206-188B-65	Sequence 65, Appli
455	61	5.1	774	3	US-09-073-259-1	Sequence 1, Appli	528	60	5.0	898	2	US-08-474-379C-12	Sequence 12, Appli
456	61	5.1	774	3	US-09-363-095-1	Sequence 1, Appli	529	60	5.0	898	3	US-09-146-249A-12	Sequence 12, Appli
457	61	5.1	774	3	US-09-418-027-1	Sequence 1, Appli	530	60	5.0	898	3	US-08-206-188B-12	Sequence 12, Appli
458	61	5.1	779	1	US-08-375-134-12	Sequence 12, Appli	531	60	5.0	900	1	US-07-688-352C-12	Sequence 12, Appli
459	61	5.1	779	5	PCT-US95-15263-12	Sequence 12, Appli	532	60	5.0	901	4	US-09-917-254-93	Sequence 93, Appli
460	61	5.1	2680	4	US-09-489-039A-7973	Sequence 7973, Ap	533	60	5.0	1037	4	US-09-252-991A-16796	Sequence 16796, A
461	61	5.1	2860	2	US-08-826-267-1	Sequence 2, Appli	534	60	5.0	1438	4	US-09-538-092-189	Sequence 189, App
462	60.5	5.0	197	4	US-09-252-991A-27889	Sequence 27889, A	535	60	5.0	1912	3	US-08-913-832A-2	Sequence 2, Appli
463	60.5	5.0	205	4	US-09-907-794A-23	Sequence 23, Appli	536	60	5.0	1912	4	US-09-249-181A-2	Sequence 2, Appli
464	60.5	5.0	205	4	US-09-905-125A-23	Sequence 23, Appli	537	60	5.0	1912	4	US-09-158-707-2	Sequence 2, Appli
465	60.5	5.0	205	4	US-09-902-775A-23	Sequence 23, Appli	538	60	5.0	2183	3	US-08-746-111-5	Sequence 5, Appli

539	5.0	2375	4	US-09-538-092-1131	Sequence 1131, Ap	612	59	4.9	769	1	US-08-477-407-4	Sequence 4, Appli
540	59.5	88	4	US-09-621-576-6877	Sequence 6877, Ap	613	59	4.9	769	1	US-08-484-355-4	Sequence 4, Appli
541	59.5	112	3	US-09-060-726A-5	Sequence 5, Appli	614	59	4.9	828	4	US-09-107-532A-4191	Sequence 4191, Ap
542	59.5	182	2	US-08-698-805-4	Sequence 4, Appli	615	59	4.9	929	4	US-09-697-022-3	Sequence 3, Appli
543	59.5	228	4	US-09-270-767-34872	Sequence 34872, A	616	59	4.9	966	2	US-08-868-786-2	Sequence 2, Appli
544	59.5	228	4	US-09-270-767-50089	Sequence 50089, A	617	59	4.9	981	2	US-08-649-046-2	Sequence 2, Appli
545	59.5	234	4	US-09-740-002-24	Sequence 24, Appl	618	59	4.9	1044	4	US-10-101-464A-956	Sequence 956, App
546	59.5	271	4	US-09-461-325-199	Sequence 199, App	619	59	4.9	1450	3	US-09-428-517-2	Sequence 2, Appli
547	59.5	271	4	US-10-012-542-199	Sequence 199, App	620	58.5	4.9	92	4	US-09-270-767-49488	Sequence 34271, A
548	59.5	271	4	US-10-115-123-199	Sequence 199, App	621	58.5	4.9	92	4	US-09-270-767-49488	Sequence 49488, A
549	59.5	306	3	US-09-392-772-6	Sequence 6, Appli	622	58.5	4.9	138	4	US-09-252-991A-17424	Sequence 17424, A
550	59.5	322	3	US-09-134-001C-3194	Sequence 3194, Ap	623	58.5	4.9	169	4	US-09-134-000C-5588	Sequence 5588, Ap
551	59.5	347	3	US-08-857-076-100	Sequence 100, App	624	58.5	4.9	182	4	US-09-489-039A-8631	Sequence 8631, Ap
552	59.5	372	4	US-09-252-991A-29108	Sequence 29108, A	625	58.5	4.9	190	4	US-09-252-991A-20976	Sequence 20976, A
553	59.5	397	4	US-09-252-991A-20113	Sequence 20113, A	626	58.5	4.9	236	1	US-08-157-101A-5	Sequence 5, Appli
554	59.5	419	4	US-09-252-991A-31409	Sequence 31409, A	627	58.5	4.9	250	4	US-09-540-236-2052	Sequence 2052, Ap
555	59.5	459	4	US-09-252-991A-26783	Sequence 26783, A	628	58.5	4.9	260	4	US-09-252-991A-29015	Sequence 29015, A
556	59.5	476	3	US-08-624-635-5	Sequence 5, Appli	629	58.5	4.9	261	4	US-09-252-991A-24007	Sequence 24007, A
557	59.5	493	4	US-09-328-352-6663	Sequence 6663, Ap	630	58.5	4.9	265	3	US-09-310-463-34	Sequence 34, Appl
558	59.5	619	4	US-09-538-092-94	Sequence 94, Appl	631	58.5	4.9	281	4	US-09-543-681A-4460	Sequence 4460, Ap
559	59.5	653	4	US-09-252-991A-16802	Sequence 16802, A	632	58.5	4.9	282	1	US-07-712-476A-5	Sequence 5, Appli
560	59.5	662	3	US-09-061-768A-25	Sequence 25, Appl	633	58.5	4.9	292	4	US-09-583-110-3511	Sequence 3511, Ap
561	59.5	662	4	US-09-764-246-25	Sequence 25, Appl	634	58.5	4.9	296	1	US-07-712-476A-1	Sequence 1, Appli
562	59.5	697	4	US-09-252-991A-32689	Sequence 32689, A	635	58.5	4.9	299	3	US-09-310-463-30	Sequence 30, Appl
563	59.5	804	3	US-08-981-446B-3	Sequence 3, Appli	636	58.5	4.9	300	6	5340934-6	Patent No. 5340934
564	59.5	1034	4	US-09-252-991A-20969	Sequence 20969, A	637	58.5	4.9	311	4	US-09-710-279-2450	Sequence 2450, Ap
565	59.5	1058	4	US-09-583-110-4522	Sequence 4522, Ap	638	58.5	4.9	312	3	US-09-821-736-5	Sequence 5, Appli
566	59.5	1261	4	US-09-248-796A-16620	Sequence 16620, A	639	58.5	4.9	314	4	US-09-134-253-1	Sequence 1, Appli
567	59.5	1992	4	US-09-538-092-1327	Sequence 1327, Ap	640	58.5	4.9	314	4	US-09-206-576-2	Sequence 2, Appli
568	59	59	4	US-09-270-767-60687	Sequence 60687, A	641	58.5	4.9	314	4	US-09-538-092-896	Sequence 896, App
569	59	111	4	US-09-149-476-673	Sequence 673, App	642	58.5	4.9	318	3	US-09-134-001C-3380	Sequence 3380, Ap
570	59	142	4	US-09-489-039A-8799	Sequence 8799, Ap	643	58.5	4.9	333	1	US-07-991-587A-2	Sequence 2, Appli
571	59	145	4	US-09-252-991A-22630	Sequence 22630, A	644	58.5	4.9	333	1	US-08-309-985-2	Sequence 2, Appli
572	59	155	3	US-09-134-001C-3243	Sequence 3243, Ap	645	58.5	4.9	344	4	US-09-270-767-43505	Sequence 43505, A
573	59	170	3	US-09-228-986-116	Sequence 116, App	646	58.5	4.9	354	4	US-09-608-917A-2	Sequence 2, Appli
574	59	170	4	US-10-101-464A-116	Sequence 116, App	647	58.5	4.9	378	3	US-09-500-569-10	Sequence 10, Appl
575	59	227	4	US-09-489-039A-10192	Sequence 10192, A	648	58.5	4.9	378	4	US-09-971-823B-10	Sequence 10, Appl
576	59	227	4	US-09-994-427A-7	Sequence 7, Appli	649	58.5	4.9	386	4	US-09-489-039A-8771	Sequence 8771, Ap
577	59	239	4	US-10-000-489-8	Sequence 8, Appli	650	58.5	4.9	400	2	US-08-624-601-8	Sequence 8, Appli
578	59	253	4	US-09-489-039A-13477	Sequence 13477, A	651	58.5	4.9	409	4	US-09-880-137-7	Sequence 7, Appli
579	59	256	4	US-09-248-796A-15990	Sequence 15990, A	652	58.5	4.9	411	4	US-09-402-532-2	Sequence 2, Appli
580	59	268	3	US-08-836-134-22	Sequence 22, Appl	653	58.5	4.9	414	4	US-09-402-532-5	Sequence 5, Appli
581	59	268	4	US-09-493-784-22	Sequence 22, Appl	654	58.5	4.9	421	3	US-09-020-846-68	Sequence 68, Appl
582	59	277	1	US-08-762-129-5	Sequence 5, Appli	655	58.5	4.9	429	4	US-09-252-991A-29792	Sequence 29792, A
583	59	295	3	US-09-037-143-50	Sequence 50, Appl	656	58.5	4.9	444	4	US-09-402-532-7	Sequence 7, Appli
584	59	295	3	US-08-260-174-50	Sequence 50, Appl	657	58.5	4.9	467	4	US-09-252-991A-27314	Sequence 27314, A
585	59	295	3	US-09-338-128A-50	Sequence 50, Appl	658	58.5	4.9	471	1	US-08-203-905B-2	Sequence 2, Appli
586	59	295	3	US-09-232-346-50	Sequence 50, Appl	659	58.5	4.9	472	1	US-08-749-901-3	Sequence 3, Appli
587	59	324	4	US-09-107-532A-6145	Sequence 6145, Ap	660	58.5	4.9	472	3	US-09-088-641-3	Sequence 3, Appli
588	59	335	4	US-09-134-000C-6145	Sequence 6145, Ap	661	58.5	4.9	477	3	US-08-704-711A-20	Sequence 20, Appl
589	59	334	4	US-09-328-859-2	Sequence 4346, Ap	662	58.5	4.9	477	3	US-08-448-489-15	Sequence 15, Appl
590	59	376	4	US-09-252-991A-17393	Sequence 2, Appli	663	58.5	4.9	477	3	US-08-281-313-1	Sequence 9, Appli
591	59	448	4	US-09-543-681A-7737	Sequence 7737, Ap	664	58.5	4.9	477	3	US-09-521-220-20	Sequence 20, Appl
592	59	469	4	US-09-252-991A-25438	Sequence 25438, A	665	58.5	4.9	477	3	US-09-391-104-21	Sequence 21, Appl
593	59	474	3	US-09-332-041-5	Sequence 5, Appli	666	58.5	4.9	481	4	US-09-543-681A-4726	Sequence 4726, Ap
594	59	479	1	US-08-313-553-7	Sequence 7, Appli	667	58.5	4.9	503	4	US-09-657-013-50	Sequence 50, Appl
595	59	479	3	US-08-767-993-7	Sequence 7, Appli	668	58.5	4.9	512	3	US-09-390-234-24	Sequence 24, Appl
596	59	506	4	US-09-489-039A-8921	Sequence 8921, Ap	669	58.5	4.9	512	3	US-09-603-311-24	Sequence 24, Appl
597	59	516	3	US-09-197-063-2	Sequence 2, Appli	670	58.5	4.9	512	4	US-09-570-856B-30	Sequence 30, Appl
598	59	530	4	US-09-252-991A-20846	Sequence 20846, A	671	58.5	4.9	549	4	US-09-657-013-54	Sequence 54, Appl
599	59	540	4	US-09-252-991A-30398	Sequence 30398, A	672	58.5	4.9	551	4	US-09-252-991A-20358	Sequence 20358, A
600	59	541	4	US-08-828-199A-2	Sequence 2, Appli	673	58.5	4.9	574	3	US-09-079-431B-6	Sequence 6, Appli
601	59	552	1	US-07-999-280A-22	Sequence 22, Appl	674	58.5	4.9	638	3	US-09-347-488-2	Sequence 2, Appli
602	59	552	1	US-08-426-279-22	Sequence 22, Appl	675	58.5	4.9	638	3	US-09-376-856-2	Sequence 2, Appli
603	59	552	1	US-08-401-013-22	Sequence 22, Appl	676	58.5	4.9	662	4	US-09-107-532A-5989	Sequence 5989, Ap
604	59	552	3	US-08-426-570-22	Sequence 22, Appl	677	58.5	4.9	721	3	US-09-390-234-20	Sequence 20, Appl
605	59	552	3	US-08-425-876-22	Sequence 22, Appl	678	58.5	4.9	721	4	US-09-603-311-20	Sequence 20, Appl
606	59	552	3	US-08-426-243-22	Sequence 22, Appl	679	58.5	4.9	731	4	US-09-252-991A-17180	Sequence 17180, A
607	59	552	3	US-08-401-632-22	Sequence 22, Appl	680	58.5	4.9	746	3	US-09-149-934-4	Sequence 4, Appli
608	59	573	4	US-09-328-352-6016	Sequence 6016, Ap	681	58.5	4.9	804	3	US-08-855-910-4	Sequence 4, Appli
609	59	573	4	US-09-489-039A-12091	Sequence 12091, A	682	58.5	4.9	848	4	US-09-538-092-33	Sequence 33, Appl
610	59	614	4	US-09-252-991A-19833	Sequence 19833, A	683	58.5	4.9	997	4	US-09-198-452A-602	Sequence 602, App
611	59	769	1	US-08-243-542-4	Sequence 4, Appli	684	58.5	4.9	1014	4	US-10-101-464A-807	Sequence 807, App

685	58.5	4.9	2584	3	US-08-936-135-4	Sequence 4, Appli	758	58	4.8	986	4	US-09-657-931A-12	Sequence 12, Appli
686	58	4.8	79	1	US-08-221-285-33	Sequence 33, Appli	759	58	4.8	1054	4	US-09-626-301-2	Sequence 2, Appli
687	58	4.8	79	3	US-08-428-596A-33	Sequence 3, Appli	760	58	4.8	1059	4	US-09-252-991A-28189	Sequence 28189, A
688	58	4.8	81	2	US-08-812-003-2	Sequence 2, Appli	761	58	4.8	1129	4	US-09-543-681A-8019	Sequence 8019, Ap
689	58	4.8	154	4	US-09-543-681A-5343	Sequence 5343, Ap	762	58	4.8	1171	4	US-09-914-272A-1	Sequence 1, Appli
690	58	4.8	158	4	US-09-252-991A-24852	Sequence 24852, A	763	58	4.8	1296	3	US-09-125-028-2	Sequence 2, Appli
691	58	4.8	160	4	US-09-252-991A-25771	Sequence 25771, A	764	58	4.8	2958	3	US-08-894-344C-2	Sequence 2, Appli
692	58	4.8	182	4	US-09-107-532A-5701	Sequence 5701, Ap	765	58	4.8	4861	4	US-09-919-497-70	Sequence 70, Appli
693	58	4.8	190	4	US-09-593-110-3050	Sequence 3050, Ap	766	58	4.8	5087	3	US-09-144-085-1	Sequence 1, Appli
694	58	4.8	191	4	US-09-538-092-118	Sequence 118, App	767	57.5	4.8	62	4	US-09-248-796A-24014	Sequence 24014, A
695	58	4.8	226	4	US-09-328-352-7169	Sequence 7169, Ap	768	57.5	4.8	132	2	US-08-616-392C-10	Sequence 10, Appl
696	58	4.8	234	3	US-09-049-672A-2	Sequence 2, Appli	769	57.5	4.8	224	4	US-09-456-090A-52	Sequence 52, Appl
697	58	4.8	241	4	US-09-270-767-42375	Sequence 42375, A	770	57.5	4.8	224	4	US-09-453-234-52	Sequence 52, Appl
698	58	4.8	251	4	US-09-489-039A-9020	Sequence 9020, Ap	771	57.5	4.8	226	4	US-09-456-090A-42	Sequence 42, Appl
699	58	4.8	262	4	US-09-270-767-57554	Sequence 57554, A	772	57.5	4.8	226	4	US-09-456-090A-80	Sequence 80, Appl
700	58	4.8	263	4	US-09-543-681A-5138	Sequence 5138, Ap	773	57.5	4.8	226	4	US-09-453-234-42	Sequence 42, Appl
701	58	4.8	272	4	US-09-328-352-7552	Sequence 7552, Ap	774	57.5	4.8	226	4	US-09-453-234-80	Sequence 80, Appl
702	58	4.8	332	4	US-09-248-796A-15797	Sequence 15797, A	775	57.5	4.8	243	4	US-09-270-767-62302	Sequence 62302, A
703	58	4.8	337	2	US-08-861-464-12	Sequence 12, Appl	776	57.5	4.8	255	4	US-09-328-352-7865	Sequence 7865, Ap
704	58	4.8	337	2	US-08-396-001-12	Sequence 12, Appl	777	57.5	4.8	257	4	US-09-248-796A-21037	Sequence 21037, A
705	58	4.8	337	3	US-09-323-433A-12	Sequence 12, Appl	778	57.5	4.8	268	4	US-09-270-767-44519	Sequence 44519, A
706	58	4.8	337	3	US-09-826-752-12	Sequence 12, Appl	779	57.5	4.8	273	4	US-09-328-352-6167	Sequence 6167, Ap
707	58	4.8	349	3	US-09-343-011B-1	Sequence 1, Appli	780	57.5	4.8	294	4	US-09-583-110-3189	Sequence 3189, Ap
708	58	4.8	351	1	US-09-324-483-2	Sequence 2, Appli	781	57.5	4.8	323	4	US-09-248-796A-15432	Sequence 15432, A
709	58	4.8	361	4	US-09-270-767-37733	Sequence 37733, A	782	57.5	4.8	335	1	US-08-085-122-13	Sequence 13, Appl
710	58	4.8	365	4	US-09-134-000C-4369	Sequence 4369, Ap	783	57.5	4.8	335	3	US-08-442-108B-23	Sequence 23, Appl
711	58	4.8	380	4	US-09-248-796A-17008	Sequence 17008, A	784	57.5	4.8	335	3	US-09-134-000C-4450	Sequence 4450, Ap
712	58	4.8	384	4	US-09-489-039A-13733	Sequence 13733, A	785	57.5	4.8	349	3	US-09-161-241-8	Sequence 8, Appli
713	58	4.8	394	4	US-09-252-991A-19674	Sequence 19674, A	786	57.5	4.8	382	4	US-09-880-137-8	Sequence 8, Appli
714	58	4.8	402	4	US-09-270-767-42272	Sequence 42272, A	787	57.5	4.8	384	4	US-09-489-039A-9127	Sequence 9127, Ap
715	58	4.8	433	4	US-09-673-899-2	Sequence 2, Appli	788	57.5	4.8	384	4	US-09-270-767-46691	Sequence 46691, A
716	58	4.8	433	4	US-09-673-899-4	Sequence 4, Appli	789	57.5	4.8	391	2	US-08-353-476-114	Sequence 114, App
717	58	4.8	433	4	US-09-673-899-6	Sequence 6, Appli	790	57.5	4.8	391	2	US-08-353-476-115	Sequence 115, App
718	58	4.8	438	4	US-09-252-991A-19012	Sequence 19012, A	791	57.5	4.8	397	3	US-09-433-248A-2	Sequence 2, Appli
719	58	4.8	438	4	US-09-538-092-62	Sequence 62, Appl	792	57.5	4.8	409	4	US-09-880-137-4	Sequence 4, Appli
720	58	4.8	443	4	US-09-540-236-3386	Sequence 3386, Ap	793	57.5	4.8	415	4	US-09-543-681A-6350	Sequence 6350, Ap
721	58	4.8	457	1	US-08-264-101-4	Sequence 4, Appli	794	57.5	4.8	416	4	US-09-328-352-6640	Sequence 6640, Ap
722	58	4.8	457	2	US-08-765-243-4	Sequence 4, Appli	795	57.5	4.8	426	4	US-09-252-991A-31959	Sequence 31959, A
723	58	4.8	457	5	PCT-US95-07295-4	Sequence 4, Appli	796	57.5	4.8	432	4	US-09-198-452A-41	Sequence 41, Appl
724	58	4.8	458	1	US-08-112-817C-2	Sequence 2, Appli	797	57.5	4.8	445	4	US-09-107-532A-5087	Sequence 5087, Ap
725	58	4.8	458	4	US-09-694-519-5	Sequence 5, Appli	798	57.5	4.8	454	3	US-08-929-323-8	Sequence 8, Appli
726	58	4.8	458	4	US-09-694-519-7	Sequence 7, Appli	799	57.5	4.8	458	3	US-09-352-168-9	Sequence 9, Appli
727	58	4.8	485	4	US-09-270-767-45701	Sequence 45701, A	800	57.5	4.8	458	4	US-09-771-045B-9	Sequence 9, Appli
728	58	4.8	486	3	US-09-082-092-10	Sequence 10, Appl	801	57.5	4.8	462	3	US-09-352-159-6	Sequence 6, Appli
729	58	4.8	496	3	US-09-288-722A-46	Sequence 46, Appl	802	57.5	4.8	462	3	US-09-352-159-8	Sequence 8, Appli
730	58	4.8	496	4	US-09-895-722A-10	Sequence 10, Appl	803	57.5	4.8	462	3	US-09-352-159-8	Sequence 8, Appli
731	58	4.8	509	4	US-09-489-039A-10350	Sequence 10350, A	804	57.5	4.8	462	3	US-09-352-168-6	Sequence 6, Appli
732	58	4.8	524	4	US-10-101-464A-943	Sequence 943, App	805	57.5	4.8	462	3	US-09-352-168-8	Sequence 8, Appli
733	58	4.8	538	4	US-09-248-796A-17632	Sequence 17632, A	806	57.5	4.8	462	4	US-09-771-045B-6	Sequence 6, Appli
734	58	4.8	541	1	US-09-583-110-2959	Sequence 2959, Ap	807	57.5	4.8	462	4	US-09-771-045B-8	Sequence 8, Appli
735	58	4.8	552	1	US-07-999-280A-24	Sequence 24, Appl	808	57.5	4.8	463	3	US-09-352-159-11	Sequence 11, Appl
736	58	4.8	552	1	US-08-426-379-24	Sequence 24, Appl	809	57.5	4.8	463	3	US-09-352-168-11	Sequence 11, Appl
737	58	4.8	552	1	US-08-401-013-24	Sequence 24, Appl	810	57.5	4.8	463	4	US-09-771-045B-11	Sequence 11, Appl
738	58	4.8	552	3	US-08-426-370-24	Sequence 24, Appl	811	57.5	4.8	463	4	US-09-771-045B-49	Sequence 49, Appl
739	58	4.8	552	3	US-08-425-876-24	Sequence 24, Appl	812	57.5	4.8	463	4	US-09-771-045B-51	Sequence 51, Appl
740	58	4.8	552	3	US-08-426-243-24	Sequence 24, Appl	813	57.5	4.8	463	4	US-09-771-045B-53	Sequence 53, Appl
741	58	4.8	552	3	US-08-401-632-24	Sequence 24, Appl	814	57.5	4.8	465	3	US-09-801-052-2	Sequence 2, Appli
742	58	4.8	563	4	US-09-540-236-2898	Sequence 2898, Ap	815	57.5	4.8	465	4	US-09-252-991A-18003	Sequence 18003, A
743	58	4.8	595	4	US-09-252-991A-25815	Sequence 25815, A	816	57.5	4.8	465	4	US-10-020-121-2	Sequence 2, Appli
744	58	4.8	630	4	US-10-003-392-16	Sequence 16, Appl	817	57.5	4.8	466	4	US-09-720-318A-8	Sequence 8, Appli
745	58	4.8	642	4	US-09-540-236-2216	Sequence 2216, Ap	818	57.5	4.8	472	3	US-09-108-020-12	Sequence 12, Appl
746	58	4.8	679	4	US-09-050-516-42	Sequence 42, Appl	819	57.5	4.8	472	3	US-09-685-296-12	Sequence 12, Appl
747	58	4.8	679	4	US-10-278-547-42	Sequence 42, Appl	820	57.5	4.8	476	3	US-09-078-173A-2	Sequence 2, Appli
748	58	4.8	729	4	US-09-328-352-7603	Sequence 7603, Ap	821	57.5	4.8	476	4	US-10-042-991-2	Sequence 2, Appli
749	58	4.8	735	2	US-08-765-243-6	Sequence 6, Appli	822	57.5	4.8	477	4	US-09-252-991A-17093	Sequence 17093, A
750	58	4.8	735	5	PCT-US95-07295-6	Sequence 6, Appli	823	57.5	4.8	480	3	US-09-078-173A-3	Sequence 3, Appli
751	58	4.8	769	4	US-09-489-039A-12201	Sequence 12201, A	824	57.5	4.8	480	4	US-10-042-991-3	Sequence 3, Appli
752	58	4.8	773	4	US-09-270-767-33141	Sequence 33141, A	825	57.5	4.8	483	3	US-09-078-173A-4	Sequence 4, Appli
753	58	4.8	773	4	US-09-270-767-48358	Sequence 48358, A	826	57.5	4.8	483	4	US-10-042-991-4	Sequence 4, Appli
754	58	4.8	808	4	US-09-270-767-36557	Sequence 36557, A	827	57.5	4.8	486	4	US-09-134-000C-4392	Sequence 4392, Ap
755	58	4.8	808	4	US-09-270-767-51774	Sequence 51774, A	828	57.5	4.8	487	3	US-09-352-159-21	Sequence 21, Appl
756	58	4.8	879	3	US-08-794-158-2	Sequence 2, Appli	829	57.5	4.8	487	3	US-09-352-168-21	Sequence 21, Appl
757	58	4.8	984	4	US-09-328-352-6926	Sequence 6926, Ap	830	57.5	4.8	487	4	US-09-771-045B-21	Sequence 21, Appl

831	57.5	4.8	488	3	US-09-078-173A-6	Sequence 6, Appli	904	57.5	4.8	1245	3	US-09-102-248-10	Sequence 10, Appli
832	57.5	4.8	488	3	US-09-537-357-38	Sequence 38, Appli	905	57.5	4.8	1245	4	US-09-367-764-3	Sequence 3, Appli
833	57.5	4.8	488	4	US-10-042-991-6	Sequence 6, Appli	906	57.5	4.8	1245	4	US-09-367-764-6	Sequence 6, Appli
834	57.5	4.8	525	4	US-10-140-002-114	Sequence 114, App	907	57.5	4.8	1245	4	US-09-367-764-10	Sequence 10, Appli
835	57.5	4.8	535	2	US-08-007-107-2	Sequence 2, Appli	908	57.5	4.8	1279	4	US-09-489-039A-13602	Sequence 13602, A
836	57.5	4.8	554	3	US-09-352-159-17	Sequence 17, Appli	909	57.5	4.8	1676	3	US-08-487-283A-2	Sequence 2, Appli
837	57.5	4.8	554	3	US-09-352-168-17	Sequence 17, Appli	910	57	4.7	110	3	US-09-060-726A-4	Sequence 4, Appli
838	57.5	4.8	554	4	US-09-771-045B-17	Sequence 17, Appli	911	57	4.7	110	4	US-09-845-849A-12	Sequence 12, Appli
839	57.5	4.8	570	3	US-08-747-221B-54	Sequence 54, Appli	912	57	4.7	119	4	US-09-489-039A-8804	Sequence 8804, Ap
840	57.5	4.8	570	3	US-09-005-051-54	Sequence 54, Appli	913	57	4.7	124	2	US-08-341-538A-4	Sequence 4, Appli
841	57.5	4.8	570	4	US-09-403-942F-54	Sequence 54, Appli	914	57	4.7	124	2	US-08-725-518-4	Sequence 4, Appli
842	57.5	4.8	592	4	US-09-252-991A-20435	Sequence 20435, A	915	57	4.7	124	2	US-09-248-796A-27788	Sequence 27788, A
843	57.5	4.8	596	3	US-08-747-221B-25	Sequence 25, Appli	916	57	4.7	135	4	US-09-489-039A-13054	Sequence 13054, A
844	57.5	4.8	596	3	US-09-005-051-25	Sequence 25, Appli	917	57	4.7	197	4	US-09-849-602-23	Sequence 23, Appli
845	57.5	4.8	596	4	US-09-403-942F-25	Sequence 25, Appli	918	57	4.7	207	2	US-08-951-822-2	Sequence 2, Appli
846	57.5	4.8	600	3	US-09-352-159-23	Sequence 23, Appli	919	57	4.7	207	3	US-09-173-043-25	Sequence 25, Appli
847	57.5	4.8	600	3	US-09-352-159-36	Sequence 36, Appli	920	57	4.7	207	3	US-09-368-951-2	Sequence 2, Appli
848	57.5	4.8	600	3	US-09-352-159-38	Sequence 38, Appli	921	57	4.7	207	4	US-09-417-721-14	Sequence 14, Appli
849	57.5	4.8	600	3	US-09-352-168-23	Sequence 23, Appli	922	57	4.7	207	4	US-09-229-947-2	Sequence 2, Appli
850	57.5	4.8	600	4	US-09-771-045B-23	Sequence 23, Appli	923	57	4.7	207	4	US-09-658-644-8	Sequence 8, Appli
851	57.5	4.8	600	4	US-09-771-045B-33	Sequence 33, Appli	924	57	4.7	234	4	US-09-472-087-17	Sequence 17, Appli
852	57.5	4.8	600	4	US-09-771-045B-36	Sequence 36, Appli	925	57	4.7	234	4	US-09-472-087-69	Sequence 69, Appli
853	57.5	4.8	600	4	US-09-771-045B-38	Sequence 38, Appli	926	57	4.7	235	3	US-08-836-236-6	Sequence 6, Appli
854	57.5	4.8	600	4	US-09-771-045B-47	Sequence 47, Appli	927	57	4.7	235	4	US-09-535-679-6	Sequence 6, Appli
855	57.5	4.8	635	3	US-09-142-623-1	Sequence 1, Appli	928	57	4.7	251	4	US-09-252-991A-32676	Sequence 32676, A
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857	57.5	4.8	648	2	US-08-478-435-109	Sequence 109, App	930	57	4.7	256	4	US-09-270-767-32813	Sequence 32813, A
858	57.5	4.8	648	2	US-08-337-483-109	Sequence 109, App	931	57	4.7	258	4	US-09-270-767-48030	Sequence 48030, A
859	57.5	4.8	648	2	US-08-478-373-109	Sequence 109, App	932	57	4.7	259	4	US-09-862-631-5	Sequence 5, Appli
860	57.5	4.8	648	3	US-08-474-671-109	Sequence 109, App	933	57	4.7	283	4	US-09-149-476-580	Sequence 580, App
861	57.5	4.8	648	3	US-08-483-578A-109	Sequence 109, App	934	57	4.7	294	4	US-09-583-110-3579	Sequence 3579, Ap
862	57.5	4.8	648	3	US-08-897-438-109	Sequence 109, App	935	57	4.7	295	4	US-09-538-092-607	Sequence 607, App
863	57.5	4.8	648	3	US-08-637-654-109	Sequence 109, App	936	57	4.7	303	4	US-09-489-039A-11076	Sequence 11076, A
864	57.5	4.8	648	3	US-08-649-518-109	Sequence 109, App	937	57	4.7	312	4	US-09-489-039A-10591	Sequence 10591, A
865	57.5	4.8	680	3	US-08-761-136-1	Sequence 1, Appli	938	57	4.7	319	4	US-09-134-000C-3600	Sequence 3600, Ap
866	57.5	4.8	680	4	US-09-576-967-1	Sequence 1, Appli	939	57	4.7	325	4	US-09-138-452A-992	Sequence 992, App
867	57.5	4.8	680	4	US-09-538-092-1165	Sequence 1165, Ap	940	57	4.7	338	4	US-09-328-352-7427	Sequence 7427, Ap
868	57.5	4.8	680	4	US-10-219-541-1	Sequence 1, Appli	941	57	4.7	347	4	US-09-710-279-3326	Sequence 3326, Ap
869	57.5	4.8	692	3	US-09-352-159-19	Sequence 19, Appli	942	57	4.7	354	3	US-09-338-907-74	Sequence 74, Appli
870	57.5	4.8	692	3	US-09-352-168-19	Sequence 19, Appli	943	57	4.7	354	3	US-09-218-207-74	Sequence 74, Appli
871	57.5	4.8	692	3	US-07-757-342D-6	Sequence 6, Appli	944	57	4.7	363	4	US-09-800-729-111	Sequence 111, App
872	57.5	4.8	692	4	US-09-461-657B-6	Sequence 6, Appli	945	57	4.7	365	4	US-09-248-796A-20986	Sequence 20986, A
873	57.5	4.8	692	4	US-09-461-657B-19	Sequence 19, Appli	946	57	4.7	366	4	US-09-750-580-3	Sequence 3, Appli
874	57.5	4.8	696	4	US-09-107-532A-3930	Sequence 3930, Ap	947	57	4.7	366	4	US-09-599-360B-89	Sequence 89, Appli
875	57.5	4.8	726	3	US-09-129-075-4	Sequence 4, Appli	948	57	4.7	366	4	US-09-800-729-212	Sequence 212, Ap
876	57.5	4.8	726	3	US-09-346-237-3	Sequence 3, Appli	949	57	4.7	371	3	US-09-134-001C-4502	Sequence 4502, Ap
877	57.5	4.8	726	3	US-09-346-237-13	Sequence 13, Appli	950	57	4.7	388	4	US-09-252-991A-30845	Sequence 30845, A
878	57.5	4.8	726	4	US-09-544-123-4	Sequence 4, Appli	951	57	4.7	398	4	US-09-248-796A-20335	Sequence 20335, A
879	57.5	4.8	808	1	US-08-471-251A-2	Sequence 2, Appli	952	57	4.7	396	4	US-09-134-000C-4226	Sequence 4226, Ap
880	57.5	4.8	826	3	US-09-564-805-2	Sequence 2, Appli	953	57	4.7	411	4	US-09-657-013-57	Sequence 57, Appli
881	57.5	4.8	829	3	US-09-352-159-33	Sequence 33, Appli	954	57	4.7	411	4	US-09-109-204-30	Sequence 30, Appli
882	57.5	4.8	829	3	US-09-352-168-33	Sequence 33, Appli	955	57	4.7	422	3	US-09-490-032-30	Sequence 30, Appli
883	57.5	4.8	842	4	US-09-489-039A-12501	Sequence 12501, A	956	57	4.7	422	4	US-09-489-039A-11341	Sequence 11341, A
884	57.5	4.8	871	4	US-09-252-991A-33057	Sequence 33057, A	957	57	4.7	446	4	US-09-870-472A-2	Sequence 2, Appli
885	57.5	4.8	903	4	US-08-252-991A-17937	Sequence 17937, A	958	57	4.7	446	4	US-09-870-472A-15	Sequence 5, Appli
886	57.5	4.8	991	3	US-09-352-159-27	Sequence 27, Appli	959	57	4.7	472	2	US-08-459-346-17	Sequence 17, Appli
887	57.5	4.8	991	3	US-09-352-168-27	Sequence 27, Appli	960	57	4.7	472	3	US-08-889-419-17	Sequence 17, Appli
888	57.5	4.8	991	4	US-09-771-045B-27	Sequence 27, Appli	961	57	4.7	472	3	US-08-402-542-17	Sequence 17, Appli
889	57.5	4.8	1000	3	US-09-352-159-25	Sequence 25, Appli	962	57	4.7	472	5	PCT-US93-07189-17	Sequence 17, Appli
890	57.5	4.8	1000	3	US-09-352-168-25	Sequence 25, Appli	963	57	4.7	475	4	US-09-543-681A-4698	Sequence 4698, Ap
891	57.5	4.8	1000	4	US-09-771-045B-25	Sequence 25, Appli	964	57	4.7	475	4	US-09-786-240-31	Sequence 31, Appli
892	57.5	4.8	1138	4	US-09-252-991A-20291	Sequence 20291, A	965	57	4.7	486	4	US-09-252-991A-25645	Sequence 25645, A
893	57.5	4.8	1196	3	US-09-352-159-31	Sequence 31, Appli	966	57	4.7	495	4	US-09-252-991A-24997	Sequence 24997, A
894	57.5	4.8	1196	3	US-09-352-168-31	Sequence 31, Appli	967	57	4.7	511	4	US-09-248-796A-16380	Sequence 16380, A
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897	57.5	4.8	1205	3	US-09-352-168-29	Sequence 29, Appli	970	57	4.7	553	1	US-08-651-572-2	Sequence 2, Appli
898	57.5	4.8	1205	4	US-09-771-045B-29	Sequence 29, Appli	971	57	4.7	553	3	US-09-066-544-2	Sequence 2, Appli
899	57.5	4.8	1245	2	US-08-801-263A-3	Sequence 3, Appli	972	57	4.7	553	3	US-08-951-086-2	Sequence 2, Appli
900	57.5	4.8	1245	2	US-08-801-263A-6	Sequence 6, Appli	973	57	4.7	553	3	US-09-430-669-2	Sequence 2, Appli
901	57.5	4.8	1245	2	US-08-801-263A-10	Sequence 10, Appli	974	57	4.7	555	4	US-09-248-796A-20471	Sequence 20471, A
902	57.5	4.8	1245	2	US-08-102-248-3	Sequence 3, Appli	975	57	4.7	559	3	US-09-442-690A-15	Sequence 15, Appli
903	57.5	4.8	1245	3	US-09-102-248-6	Sequence 6, Appli	976	57	4.7	559	3	US-09-298-924-6	Sequence 6, Appli

977	57	4.7	559	4	US-09-908-855-15	Sequence 15, Appl	1050	56.5	4.7	250	3	US-09-134-001C-2869	Sequence 2869, Ap
978	57	4.7	630	3	US-08-860-091A-2	Sequence 2, Appl	1051	56.5	4.7	272	4	US-09-252-991A-19844	Sequence 19844, A
979	57	4.7	630	3	US-09-245-323A-6	Sequence 6, Appl	1052	56.5	4.7	274	4	US-09-808-701A-31	Sequence 31, Appl
980	57	4.7	630	4	US-10-003-392-18	Sequence 18, Appl	1053	56.5	4.7	291	4	US-09-252-991A-28755	Sequence 28755, A
981	57	4.7	631	4	US-09-107-532A-6577	Sequence 6577, Ap	1054	56.5	4.7	293	4	US-09-720-318A-2	Sequence 2, Appl
982	57	4.7	633	4	US-09-489-039A-11853	Sequence 11853, A	1055	56.5	4.7	307	3	US-09-105-390-42	Sequence 42, Appl
983	57	4.7	666	1	US-08-083-590A-17	Sequence 17, Appl	1056	56.5	4.7	309	1	US-08-078-683A-5	Sequence 5, Appl
984	57	4.7	666	2	US-08-346-128-36	Sequence 36, Appl	1057	56.5	4.7	309	4	US-08-471-970A-5	Sequence 5, Appl
985	57	4.7	666	3	US-08-532-384-17	Sequence 17, Appl	1058	56.5	4.7	309	4	US-09-723-677B-5	Sequence 5, Appl
986	57	4.7	682	1	US-07-998-003A-107	Sequence 107, App	1059	56.5	4.7	310	4	US-10-140-002-152	Sequence 152, App
987	57	4.7	682	1	US-08-453-274B-107	Sequence 107, App	1060	56.5	4.7	319	4	US-09-543-681A-4976	Sequence 4976, Ap
988	57	4.7	682	1	US-08-453-695A-107	Sequence 107, App	1061	56.5	4.7	319	4	US-09-543-681A-4976	Sequence 2871, Ap
989	57	4.7	682	1	US-08-268-161A-107	Sequence 107, App	1062	56.5	4.7	322	4	US-09-540-236-2871	Sequence 5520, Ap
990	57	4.7	682	2	US-08-453-702A-107	Sequence 107, App	1063	56.5	4.7	332	3	US-09-107-532A-5520	Sequence 58, Appl
991	57	4.7	682	3	US-09-039-639-107	Sequence 107, App	1064	56.5	4.7	333	3	US-09-105-390-58	Sequence 58, Appl
992	57	4.7	682	5	PCT-US93-12588-107	Sequence 107, App	1065	56.5	4.7	350	3	US-09-413-231-10	Sequence 10, Appl
993	57	4.7	682	5	PCT-US95-08071-107	Sequence 107, App	1066	56.5	4.7	350	3	US-09-161-241-9	Sequence 9, Appl
994	57	4.7	754	4	US-09-300-008B-2	Sequence 2, Appl	1067	56.5	4.7	350	4	US-09-907-794A-236	Sequence 236, App
995	57	4.7	758	4	US-09-328-352-4521	Sequence 4521, Ap	1068	56.5	4.7	350	4	US-09-905-125A-236	Sequence 236, App
996	57	4.7	829	3	US-09-514-599-6	Sequence 6, Appl	1069	56.5	4.7	350	4	US-09-902-775A-236	Sequence 236, App
997	57	4.7	830	4	US-09-064-199-19	Sequence 19, Appl	1070	56.5	4.7	350	4	US-09-906-700-236	Sequence 236, App
998	57	4.7	836	1	US-07-998-003A-105	Sequence 105, App	1071	56.5	4.7	351	4	US-09-903-603A-236	Sequence 236, App
999	57	4.7	836	1	US-08-453-274B-105	Sequence 105, App	1072	56.5	4.7	351	4	US-09-857-447-1	Sequence 1, Appl
1000	57	4.7	836	1	US-08-453-695A-105	Sequence 105, App	1073	56.5	4.7	375	4	US-09-328-352-6262	Sequence 6262, Ap
1001	57	4.7	836	1	US-08-268-161A-105	Sequence 105, App	1074	56.5	4.7	376	4	US-09-328-352-8084	Sequence 8084, Ap
1002	57	4.7	836	2	US-08-453-702A-105	Sequence 105, App	1075	56.5	4.7	379	4	US-09-402-532-3	Sequence 3, Appl
1003	57	4.7	836	3	US-09-039-639-105	Sequence 105, App	1076	56.5	4.7	391	4	US-09-543-681A-7029	Sequence 7029, Ap
1004	57	4.7	836	5	PCT-US93-12588-105	Sequence 105, App	1077	56.5	4.7	398	4	US-09-248-796A-25567	Sequence 25567, A
1005	57	4.7	836	5	PCT-US95-08071-105	Sequence 105, App	1078	56.5	4.7	398	4	US-09-252-991A-25295	Sequence 25295, A
1006	57	4.7	862	3	US-09-346-237-1	Sequence 1, Appl	1079	56.5	4.7	412	4	US-09-402-532-8	Sequence 8, Appl
1007	57	4.7	873	2	US-08-912-129A-61	Sequence 61, Appl	1080	56.5	4.7	437	4	US-09-252-991A-24390	Sequence 24390, A
1008	57	4.7	879	1	US-08-072-574-6	Sequence 6, Appl	1081	56.5	4.7	449	3	US-09-293-505-29	Sequence 29, Appl
1009	57	4.7	879	1	US-08-486-270-6	Sequence 6, Appl	1082	56.5	4.7	449	4	US-09-060-939A-29	Sequence 29, Appl
1010	57	4.7	879	3	US-08-367-264-6	Sequence 6, Appl	1083	56.5	4.7	472	4	US-09-720-318A-6	Sequence 6, Appl
1011	57	4.7	879	4	US-08-153-757-6	Sequence 6, Appl	1084	56.5	4.7	476	4	US-09-489-039A-12217	Sequence 12217, A
1012	57	4.7	885	4	US-09-459-715-6	Sequence 6, Appl	1085	56.5	4.7	500	4	US-09-354-123-6	Sequence 6, Appl
1013	57	4.7	885	2	US-08-577-492-33	Sequence 33, Appl	1086	56.5	4.7	511	4	US-09-198-452A-509	Sequence 509, App
1014	57	4.7	885	3	US-09-079-630-33	Sequence 33, Appl	1087	56.5	4.7	523	4	US-09-107-532A-4149	Sequence 4149, App
1015	57	4.7	904	1	US-07-998-003A-97	Sequence 97, Appl	1088	56.5	4.7	528	4	US-09-252-991A-18286	Sequence 18286, A
1016	57	4.7	904	1	US-08-453-274B-97	Sequence 97, Appl	1089	56.5	4.7	543	2	US-08-808-931-12	Sequence 12, Appl
1017	57	4.7	904	1	US-08-453-695A-97	Sequence 97, Appl	1090	56.5	4.7	543	3	US-09-050-603A-12	Sequence 12, Appl
1018	57	4.7	904	1	US-08-268-161A-97	Sequence 97, Appl	1091	56.5	4.7	543	3	US-09-102-420B-12	Sequence 12, Appl
1019	57	4.7	904	2	US-08-453-702A-97	Sequence 97, Appl	1092	56.5	4.7	543	3	US-09-497-698-12	Sequence 12, Appl
1020	57	4.7	904	3	US-09-039-639-97	Sequence 97, Appl	1093	56.5	4.7	543	4	US-09-302-357-6	Sequence 6, Appl
1021	57	4.7	904	5	PCT-US93-12588-97	Sequence 97, Appl	1094	56.5	4.7	557	4	US-09-568-816A-2	Sequence 2, Appl
1022	57	4.7	904	5	PCT-US95-08071-97	Sequence 97, Appl	1095	56.5	4.7	574	3	US-09-142-623-13	Sequence 13, Appl
1023	57	4.7	951	4	US-09-252-991A-23338	Sequence 23338, A	1096	56.5	4.7	575	4	US-09-394-142B-20	Sequence 20, Appl
1024	57	4.7	1106	4	US-09-064-199-17	Sequence 17, Appl	1097	56.5	4.7	613	4	US-09-508-264A-3	Sequence 3, Appl
1025	57	4.7	1130	2	US-08-519-547A-6	Sequence 6, Appl	1098	56.5	4.7	619	4	US-09-252-991A-32940	Sequence 32940, A
1026	57	4.7	1130	4	US-09-064-199-18	Sequence 18, Appl	1099	56.5	4.7	677	4	US-09-394-142B-6	Sequence 6, Appl
1027	57	4.7	1207	4	US-09-064-199-16	Sequence 16, Appl	1100	56.5	4.7	682	4	US-09-252-991A-24919	Sequence 24919, A
1028	57	4.7	1225	4	US-09-252-991A-25018	Sequence 25018, A	1101	56.5	4.7	769	3	US-08-434-000A-10	Sequence 10, Appl
1029	57	4.7	1287	4	US-08-325-547-3	Sequence 2958, A	1102	56.5	4.7	769	3	US-09-312-157-10	Sequence 10, Appl
1030	57	4.7	1324	2	US-08-811-897A-56	Sequence 56, Appl	1103	56.5	4.7	773	4	US-09-252-991A-19916	Sequence 19916, A
1031	57	4.7	1324	3	US-09-201-474-56	Sequence 56, Appl	1104	56.5	4.7	826	3	US-09-564-805-224	Sequence 224, App
1032	57	4.7	1724	1	US-08-325-547-3	Sequence 3, Appl	1105	56.5	4.7	832	4	US-09-538-093-88	Sequence 88, Appl
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1040	56.5	4.7	224	4	US-09-456-090A-78	Sequence 78, Appl	1113	56.5	4.7	1068	1	US-09-966-997-11	Sequence 11, Appl
1041	56.5	4.7	224	4	US-09-453-234-44	Sequence 44, Appl	1114	56.5	4.7	1078	1	US-08-485-588-7	Sequence 7, Appl
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1172	56	4.7	333	3	US-09-073-297-3	Sequence 3, Appli	1245	55.5	4.6	215	4	US-09-270-767-45569	Sequence 45569, A
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1181	56	4.7	403	4	US-09-543-681A-5377	Sequence 5377, Ap	1254	55.5	4.6	301	4	US-09-489-039A-12472	Sequence 12472, A
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1191	56	4.7	512	4	US-09-464-377-9	Sequence 9, Appli	1264	55.5	4.6	365	4	US-09-149-476-696	Sequence 696, App
1192	56	4.7	520	4	US-09-583-110-3457	Sequence 3457, Ap	1265	55.5	4.6	365	4	US-09-010-147B-24	Sequence 24, Appl
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1276	55.5	4.6	401	4	US-08-577-788C-4	Sequence 4, Appli	1349	55.5	4.6	1402	4	US-09-125-635-12	Sequence 12, Appl
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1279	55.5	4.6	410	4	US-09-676-475A-452	Sequence 452, App	1352	55.5	4.6	1584	3	US-09-251-645-6	Sequence 6, Appli
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1282	55.5	4.6	415	5	PCT-US92-10243-2	Sequence 2, Appli	1355	55.5	4.6	3144	1	US-08-453-265-6	Sequence 6, Appli
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1286	55.5	4.6	462	2	US-09-051-342-1	Sequence 1, Appli	1359	55.5	4.6	3144	3	US-09-041-886-15	Sequence 15, Appl
1287	55.5	4.6	462	3	US-08-468-161-1	Sequence 1, Appli	1360	55.5	4.6	3168	4	US-09-538-092-1118	Sequence 1118, Ap
1288	55.5	4.6	462	3	US-09-051-759-1	Sequence 1, Appli	1361	55.5	4.6	15281	2	US-09-489-039A-14067	Sequence 14067, A
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1290	55.5	4.6	469	4	US-09-489-039A-10553	Sequence 10553, A	1363	55	4.6	69	1	US-08-403-378B-7	Sequence 7, Appli
1291	55.5	4.6	469	4	US-09-252-991A-31978	Sequence 31978, A	1364	55	4.6	72	1	US-08-244-702-3	Sequence 3, Appli
1292	55.5	4.6	472	4	US-09-328-352-7877	Sequence 7877, Ap	1365	55	4.6	73	1	US-08-482-111-47	Sequence 47, Appl
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1296	55.5	4.6	487	4	US-09-270-767-39873	Sequence 39873, A	1369	55	4.6	141	2	US-08-411-726-5	Sequence 5, Appli
1297	55.5	4.6	487	4	US-09-270-767-55090	Sequence 55090, A	1370	55	4.6	141	6	5217896-3	Patent No. 5217896
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1301	55.5	4.6	490	4	US-10-012-542-250	Sequence 250, App	1374	55	4.6	177	4	US-09-643-597-165	Sequence 165, App
1302	55.5	4.6	490	4	US-10-115-123-250	Sequence 250, App	1375	55	4.6	177	4	US-09-643-597-165	Sequence 165, App
1303	55.5	4.6	490	4	US-10-115-123-250	Sequence 250, App	1376	55	4.6	177	4	US-09-480-884A-165	Sequence 165, App
1304	55.5	4.6	492	3	US-09-794-236-2	Sequence 2, Appli	1377	55	4.6	177	4	US-09-480-884A-165	Sequence 165, App
1305	55.5	4.6	492	3	US-09-345-469-1	Sequence 1, Appli	1378	55	4.6	177	4	US-09-542-615A-165	Sequence 165, App
1306	55.5	4.6	515	4	US-08-476-123-12	Sequence 12, Appl	1379	55	4.6	177	4	US-09-542-615A-165	Sequence 165, App
1307	55.5	4.6	515	4	US-09-461-325-219	Sequence 219, App	1380	55	4.6	177	4	US-09-606-421B-165	Sequence 165, App
1308	55.5	4.6	515	4	US-10-012-542-219	Sequence 219, App	1381	55	4.6	177	4	US-09-606-421B-165	Sequence 165, App
1309	55.5	4.6	519	4	US-09-328-352-7681	Sequence 7681, Ap	1382	55	4.6	177	4	US-09-976-594-447	Sequence 447, App
1310	55.5	4.6	519	4	US-09-328-352-7681	Sequence 7681, Ap	1383	55	4.6	177	4	US-09-466-396A-165	Sequence 165, App
1311	55.5	4.6	526	4	US-09-252-991A-21586	Sequence 21586, A	1384	55	4.6	177	4	US-09-466-396A-165	Sequence 165, App
1312	55.5	4.6	537	4	US-09-388-413B-6	Sequence 6, Appli	1385	55	4.6	177	4	US-09-476-496A-165	Sequence 165, App
1313	55.5	4.6	537	4	US-10-233-745-6	Sequence 6, Appli	1386	55	4.6	177	4	US-09-476-496A-165	Sequence 165, App
1314	55.5	4.6	542	3	US-08-935-855-22	Sequence 22, Appl	1387	55	4.6	177	4	US-09-630-940B-165	Sequence 165, App
1315	55.5	4.6	550	4	US-09-252-991A-19086	Sequence 19086, A	1388	55	4.6	177	4	US-09-630-940B-165	Sequence 165, App
1316	55.5	4.6	561	2	US-08-756-317-14	Sequence 14, Appl	1389	55	4.6	203	1	US-09-248-796A-27919	Sequence 27919, A
1317	55.5	4.6	565	2	US-08-700-548-2	Sequence 2, Appli	1390	55	4.6	209	1	US-08-664-111C-1	Sequence 1, Appli
1318	55.5	4.6	567	4	US-09-711-164-409	Sequence 409, App	1391	55	4.6	224	4	US-09-456-090A-84	Sequence 84, Appl
1319	55.5	4.6	568	4	US-09-252-991A-27039	Sequence 27039, A	1392	55	4.6	224	4	US-09-453-234-84	Sequence 84, Appl
1320	55.5	4.6	575	4	US-09-248-796A-17507	Sequence 17507, A	1393	55	4.6	227	4	US-09-270-767-43391	Sequence 43391, A
1321	55.5	4.6	599	4	US-09-252-991A-29067	Sequence 29067, A	1394	55	4.6	235	3	US-08-812-586-16	Sequence 16, Appl
1322	55.5	4.6	610	2	US-08-896-344A-2	Sequence 2, Appli	1395	55	4.6	235	4	US-09-535-832A-17	Sequence 17, Appl
1323	55.5	4.6	610	3	US-09-360-682A-2	Sequence 2, Appli	1396	55	4.6	235	4	US-09-472-087-14	Sequence 14, Appl
1324	55.5	4.6	630	4	US-08-472-888A-6	Sequence 6, Appli	1397	55	4.6	235	4	US-09-472-087-65	Sequence 65, Appl
1325	55.5	4.6	635	4	US-09-252-991A-33100	Sequence 33100, A	1398	55	4.6	245	3	US-08-944-483-69	Sequence 69, Appl
1326	55.5	4.6	679	3	US-09-257-536-2	Sequence 2, Appli	1399	55	4.6	252	1	US-07-717-332D-2	Sequence 2, Appli
1327	55.5	4.6	679	3	US-09-512-230-2	Sequence 2, Appli	1400	55	4.6	252	5	PCT-US96-01314-56	Sequence 56, Appl
1328	55.5	4.6	708	4	US-09-252-991A-20021	Sequence 20021, A	1401	55	4.6	252	4	US-09-270-767-46084	Sequence 46084, A
1329	55.5	4.6	717	4	US-09-489-039A-13855	Sequence 13855, A	1402	55	4.6	282	3	US-08-558-207A-350	Sequence 350, App
1330	55.5	4.6	771	3	US-08-434-000A-8	Sequence 8, Appli	1403	55	4.6	288	4	US-09-489-039A-8883	Sequence 8883, Ap
1331	55.5	4.6	771	3	US-09-312-157-8	Sequence 8, Appli	1404	55	4.6	288	4	US-09-270-767-44078	Sequence 44078, A
1332	55.5	4.6	774	4	US-09-489-039A-11783	Sequence 11783, A	1405	55	4.6	290	4	US-09-583-110-2707	Sequence 2707, Ap
1333	55.5	4.6	784	4	US-09-583-110-5192	Sequence 5192, Ap	1406	55	4.6	297	3	US-08-845-258-26	Sequence 26, Appl
1334	55.5	4.6	826	3	US-09-564-805-226	Sequence 226, App	1407	55	4.6	297	3	US-08-950-571-26	Sequence 26, Appl
1335	55.5	4.6	834	4	US-09-252-991A-32671	Sequence 32671, A	1408	55	4.6	297	4	US-09-528-784A-26	Sequence 26, Appl
1336	55.5	4.6	889	4	US-09-252-991A-30096	Sequence 30096, A	1409	55	4.6	311	1	US-09-569-098A-26	Sequence 26, Appl
1337	55.5	4.6	933	3	US-09-141-206-2	Sequence 2, Appli	1410	55	4.6	311	1	US-08-872-784-1	Sequence 1, Appli
1338	55.5	4.6	998	4	US-09-198-452A-841	Sequence 841, App	1411	55	4.6	311	2	US-09-100-951-1	Sequence 1, Appli
1339	55.5	4.6	1067	4	US-09-252-991A-19697	Sequence 19697, A	1412	55	4.6	311	3	US-09-265-294-1	Sequence 1, Appli
1340	55.5	4.6	1079	1	US-08-485-588-8	Sequence 8, Appli	1413	55	4.6	312	4	US-09-248-796A-14231	Sequence 14231, A
1341	55.5	4.6	1079	1	US-08-484-565-8	Sequence 8, Appli	1414	55	4.6	312	4	US-09-248-796A-14231	Sequence 14231, A

QY 61 VPDNNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAEPRQRFWRHVLVTDIKG 120
DB 61 VPDNNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAEPRQRFWRHVLVTDIKG 120
QY 121 ADLKGKIQOELSAYQAPSPAHSGFHRFYQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
DB 121 ADLKGKIQOELSAYQAPSPAHSGFHRFYQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
QY 181 LNRFLHGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTR 221
DB 181 LNRFLHGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTR 221

RESULT 2
US-09-621-976-8
; Sequence 8, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; LOCATION: -22...-1
US-09-621-976-8

Query Match 97.8%; Score 1177; DB 4; Length 227;
Best Local Similarity 98.6%; Pred. No. 2.8e-124;
Matches 218; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGWTMLRVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
DB 1 MGWTMLRVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
QY 61 VPDNNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAEPRQRFWRHVLVTDIKG 120
DB 61 VPDNNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAEPRQRFWRHVLVTDIKG 120
QY 121 ADLKGKIQOELSAYQAPSPAHSGFHRFYQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
DB 121 ADLKGKIQOELSAYQAPSPAHSGFHRFYQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
QY 181 LNRFLHGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTR 221
DB 181 LNRFLHGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTR 221

RESULT 3
US-09-513-999C-8
; Sequence 8, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 8
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; LOCATION: -22...-1
; OTHER INFORMATION: score 8.5
; OTHER INFORMATION: seq AALLGLMMVVTG/DE
US-09-513-999C-8

Query Match 97.8%; Score 1177; DB 4; Length 227;
Best Local Similarity 98.6%; Pred. No. 2.8e-124;
Matches 218; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGWTMLRVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
DB 1 MGWTMLRVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
QY 61 VPDNNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAEPRQRFWRHVLVTDIKG 120
DB 61 VPDNNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAEPRQRFWRHVLVTDIKG 120
QY 121 ADLKGKIQOELSAYQAPSPAHSGFHRFYQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
DB 121 ADLKGKIQOELSAYQAPSPAHSGFHRFYQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
QY 181 LNRFLHGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTR 221
DB 181 LNRFLHGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTR 221

RESULT 4
US-09-492-308A-7
; Sequence 7, Application US/09492308A
; Patent No. 6573430
; GENERAL INFORMATION:
; APPLICANT: Bradley, DJ
; Carpenter, R
; Coen, ES
; TITLE OF INVENTION: Flowering genes
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 8th Floor, 1100 No. 6573430th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/492,308A
; FILING DATE: 27-Jan-2000
; CLASSIFICATION: 435 (Preliminary)
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/043,029
; FILING DATE: 13-MAR-1998
; APPLICATION NUMBER: PCT/GB96/02276
; FILING DATE: 13-SEP-1996
; APPLICATION NUMBER: GB 9518731.6
; FILING DATE: 13-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary J. Wilson
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 620-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000


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; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-492-308A-7

Query Match 19.6%; Score 235.5; DB 4; Length 187;
Best Local Similarity 36.5%; Pred. No. 2.2e-18;
Matches 57; Conservative 20; Mismatches 60; Indels 19; Gaps 5;

Qy 52 ELNIGCKVDPDCNNYRQKITSWMEPIVKFPGAVDGTATYILVMVDDPAPRAEPRQRFR 111
Db 36 ELGKV---LTPTQVMNRPSISW-----DGLDPGKLYTLVLTDPDAPSRKDKPFREWH 85

Qy 112 HMLVTIDKAGDLKKGIOGQELSAYQAPSPAHSGFHRYPFFVYLQSGKVIS-----LLPK 167
Db 86 HFLVNNKGNDISGTV-----LSYVGGPPKDTGLHRYVWLVTYEQSPLNCDPEILSNK 141

Qy 168 ENKTRGSKMDRFLNRFHLGPEASTQFMNTQYQDS 203
Db 142 SGDNRGKFKVESFRKXKYLGAAPVAGTCQAE-WDS 176

RESULT 5
US-09-208-718-6
; Sequence 6, Application US/09208718
; Patent No. 6063767
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer
; APPLICANT: Corley, Neil
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN PHOSPHOLIPID BINDING PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/208,718
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,820
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0379 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1143527
US-09-208-718-6

Query Match 19.6%; Score 235.5; DB 4; Length 187;
Best Local Similarity 36.5%; Pred. No. 2.2e-18;
Matches 57; Conservative 20; Mismatches 60; Indels 19; Gaps 5;

Qy 52 ELNIGCKVDPDCNNYRQKITSWMEPIVKFPGAVDGTATYILVMVDDPAPRAEPRQRFR 111
Db 36 ELGKV---LTPTQVMNRPSISW-----DGLDPGKLYTLVLTDPDAPSRKDKPFREWH 85

Qy 112 HMLVTIDKAGDLKKGIOGQELSAYQAPSPAHSGFHRYPFFVYLQSGKVIS-----LLPK 167
Db 86 HFLVNNKGNDISGTV-----LSYVGGPPKDTGLHRYVWLVTYEQSPLNCDPEILSNK 141

Qy 168 ENKTRGSKMDRFLNRFHLGPEASTQFMNTQYQDS 203
Db 142 SGDNRGKFKVESFRKXKYLGAAPVAGTCQAE-WDS 176

RESULT 6
US-09-492-308A-8
; Sequence 8, Application US/09492308A
; Patent No. 6573430
; GENERAL INFORMATION:
; APPLICANT: Bradley, DJ
; APPLICANT: Carpenter, R
; APPLICANT: Coen, ES
; TITLE OF INVENTION: Flowering genes
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 8th Floor, 1100 No. 6573430th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/492,308A
; FILING DATE: 27-Jan-2000
; CLASSIFICATION: 435 (Preliminary)
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/043,029
; FILING DATE: 13-MAR-1998
; APPLICATION NUMBER: PCT/GB96/02276
; FILING DATE: 13-SEP-1996
; APPLICATION NUMBER: GB 9518731.6
; FILING DATE: 13-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary J. Wilson
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 620-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 186 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-492-308A-8

Query Match 18.1%; Score 218.5; DB 4; Length 186;
Best Local Similarity 33.3%; Pred. No. 1.8e-16;
Matches 53; Conservative 24; Mismatches 65; Indels 17; Gaps 4;

Qy 46 LEVFF--PELGNIGCKVDPDCNNYRQKITSWMEPIVKFPGAVDGTATYILVMVDDPAPRA 103
Db 24 LQVKGGAEDVDELGKVLTPQVKNRPTSIW-----DGLDPGKLYTLVLTDPDAPSRK 76
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TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-403-378B-4

Query Match 17.5%; Score 210.5; DB 1; Length 187;
Best Local Similarity 36.3%; Pred. No. 1.5e-15;
Matches 57; Conservative 20; Mismatches 59; Indels 21; Gaps 7;

QY 52 ELGNIGCKVDPDNNYRQKITSMPEIVKFPFCVADGATYILVMVDPDAPSRAEPRQRPWR 111
DB 36 ELGKV---LTPQVNRPSISW-----DGLDPGLYTLVLTDPDAPSRKDPKFRWH 85
QY 112 HVLVTDIKADLKKIKQOELSAYQAPSPAHSGFH-RYQFFVYLOEGKVIS-----LLP 166
DB 86 HFLVVMKGNDISGTV---LSEY-VGSGPRDTGLHRYVWLVEQOPLNCDEPILSN 140
QY 167 KENKTRGSKWMDRFLNRFLHGLGEPEASTQFTQVODS 203
DB 141 KSGDNRGKFKVESFRKKYHLGAPVAGTCFQAE-WDDS 176

RESULT 8
US-08-403-378B-15
Sequence 15, Application US/08403378B
Patent No. 5759991
GENERAL INFORMATION:
APPLICANT: TOHDOH, NAOKI
APPLICANT: TOJO, SHIN-ICHIRO
APPLICANT: KOJIMA, SHIN-ICHI
APPLICANT: UEKI, YASUYUKI
APPLICANT: NISHIHARA, TOSHIO
APPLICANT: FUKUSHIMA, NOBUYUKI
APPLICANT: IRIE, TSUNEMASA
APPLICANT: ONO, KEIICHI
APPLICANT: AGUI, HIDEO
APPLICANT: OJIKI, KOSEI
TITLE OF INVENTION: NEUTROTROPIC PEPTIDE DERIVATIVES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 PENNSYLVANIA AVENUE, NW
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403.378B
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-124688
FILING DATE: 27-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-080398
FILING DATE: 30-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-280590
FILING DATE: 27-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-333241
FILING DATE: 21-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-243003
FILING DATE: 12-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/758,043
FILING DATE: 12-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/873,764
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/01214
FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: BIGGART, WADDELL A
REGISTRATION NUMBER: 24,861
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060

104 EPRQFRHVLVTDIKGADLKKIKQOELSAYQAPSPAHSGFHRHYQFFVYLOEGKVIS 163
77 DPKYREWHFLVNMKGNISSGTV---LSDYVSGPFGTGLHRYVWLVEQEGPLKC 132
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133 DEPILSNRSGDRHGKFKVASFRKKYELGAPVAGTCYQAE 171

RESULT 7
US-08-403-378B-4
Sequence 4, Application US/08403378B
Patent No. 5759991
GENERAL INFORMATION:
APPLICANT: TOHDOH, NAOKI
APPLICANT: TOJO, SHIN-ICHIRO
APPLICANT: KOJIMA, SHIN-ICHI
APPLICANT: UEKI, YASUYUKI
APPLICANT: NISHIHARA, TOSHIO
APPLICANT: FUKUSHIMA, NOBUYUKI
APPLICANT: IRIE, TSUNEMASA
APPLICANT: ONO, KEIICHI
APPLICANT: AGUI, HIDEO
APPLICANT: OJIKI, KOSEI
TITLE OF INVENTION: NEUTROTROPIC PEPTIDE DERIVATIVES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 PENNSYLVANIA AVENUE, NW
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403.378B
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-124688
FILING DATE: 27-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-080398
FILING DATE: 30-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-280590
FILING DATE: 27-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-333241
FILING DATE: 21-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-243003
FILING DATE: 12-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/758,043
FILING DATE: 12-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/873,764
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/01214
FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: BIGGART, WADDELL A
REGISTRATION NUMBER: 24,861
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060


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US-09-248-796A-16385
; Sequence 16385, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16385
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-16385

Query Match 13.0%; Score 157; DB 4; Length 272;
Best Local Similarity 29.9%; Pred. No. 2.6e-09;
Matches 38; Conservative 23; Mismatches 46; Indels 20; Gaps 3;

Qy 90 YILVMDPDAPSRAEPRQFRWHLVTDIK-----GADLKKGKIQOELS 134
Db 142 FILVMTDPDAPNSDKHWSYHLWLTDLKLPHTKQEDGEPFISHFIDVK---EGRELV 197

Qy 135 AYQAPSPAHSGHRYOFFVYLOGKVISL-LPKNKTRGSKWMDRFLNRFHLGPEAST 193
Db 198 PYMGPGPPKRGHRYVFLLYKQDPNAGELTAPGRPKGLLDYQAVVSKDWVEKATNS 257

Qy 194 QFMTONY 200
Db 258 KLLSVNF 264

RESULT 13
US-09-492-308A-2
; Sequence 2, Application US/09492308A
; Patent No. 6573430
; GENERAL INFORMATION:
; APPLICANT: Bradley, DJ
; Carpenter, R
; Coen, ES
; TITLE OF INVENTION: Flowering genes
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 8th Floor, 1100 No. 6573430th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22201-4714
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/492,308A
; FILING DATE: 27-Jan-2000
; CLASSIFICATION: 435 (Preliminary)
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/043,029
; FILING DATE: 13-MAR-1998
; APPLICATION NUMBER: PCT/GB96/02276
; FILING DATE: 13-SEP-1996
; APPLICATION NUMBER: GB 9518731.6
; FILING DATE: 13-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary J. Wilson
;

US-09-492-308A-23
; Sequence 23, Application US/09492308A
; Patent No. 6573430
; GENERAL INFORMATION:
; APPLICANT: Bradley, DJ
; Carpenter, R
; Coen, ES
; TITLE OF INVENTION: Flowering genes
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 8th Floor, 1100 No. 6573430th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22201-4714
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/492,308A
; FILING DATE: 27-Jan-2000
; CLASSIFICATION: 435 (Preliminary)
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/043,029
; FILING DATE: 13-MAR-1998
; APPLICATION NUMBER: PCT/GB96/02276
; FILING DATE: 13-SEP-1996
; APPLICATION NUMBER: GB 9518731.6
; FILING DATE: 13-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary J. Wilson
;

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; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 620-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Antirrhinum majus
; CLONE: CEN PROTEIN
; IMMEDIATE SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-492-308A-2

Query Match 12.3%; Score 148; DB 4; Length 181;
Best Local Similarity 29.1%; Pred. No. 1.5e-08;
Matches 44; Conservative 25; Mismatches 62; Indels 20; Gaps 5;

Qy 60 VVPDCNN-----YRQKITSWMEPIVKFPGAVDGTATYILVMDPDAPSRAEPROR 108
Db 31 VIVNSNNSIKHYVNGHELFPSPAVTS--TPRVEVHGDMRSFETLIMTDPDVPGSDPYLR 88

Qy 109 FWRHLVTDIKG-ADLKKGKIQOELSAYQAPSPAHSGHRYOFFVYLOGKVISLLPK 167
Db 89 EHLWITVTDIPGTTDSSFGK---EVVSYEMPRP--NIGIHRFVLLFKQKRGQAMLSF 142

Qy 168 ENKTGSKWMDRFLNRFHLGPEASTQFMTO 198
Db 143 PVVCRDGFNTRKFTQENELGLPVAUVFNCQ 173

RESULT 14
US-09-492-308A-23
; Sequence 23, Application US/09492308A
; Patent No. 6573430
; GENERAL INFORMATION:
; APPLICANT: Bradley, DJ
; Carpenter, R
; Coen, ES
; TITLE OF INVENTION: Flowering genes
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 8th Floor, 1100 No. 6573430th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22201-4714
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/492,308A
; FILING DATE: 27-Jan-2000
; CLASSIFICATION: 435 (Preliminary)
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/043,029
; FILING DATE: 13-MAR-1998
; APPLICATION NUMBER: PCT/GB96/02276
; FILING DATE: 13-SEP-1996
; APPLICATION NUMBER: GB 9518731.6
; FILING DATE: 13-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary J. Wilson
;

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